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(54) **MICROORGANISMS FOR
C4-DICARBOXYLIC ACID PRODUCTION**

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C12P 7/46 (2006.01)

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(52) **U.S. Cl.**

CPC **C12P 7/46** (2013.01); **C07K 14/38**
(2013.01); **C12N 1/14** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

The present invention relates to isolated polypeptides having bicarbonate transporter activity and isolated polynucleotides encoding the polypeptides. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the polynucleotides as well as methods of producing and using the polypeptides, and methods of producing C4-dicarboxylic acids, such as malic acid.

30 Claims, 15 Drawing Sheets

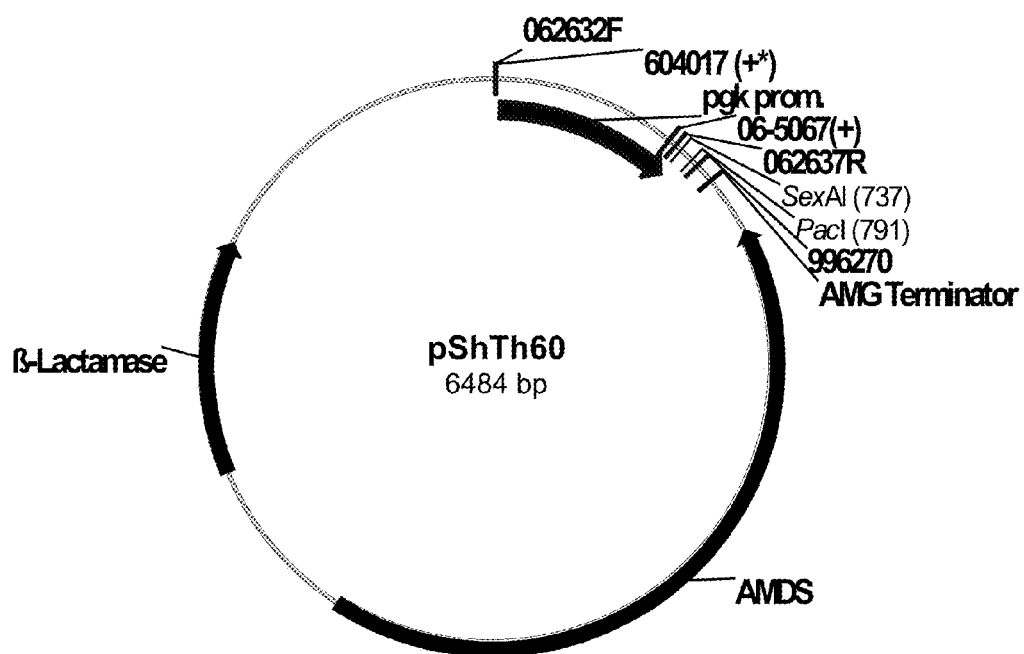


Fig. 1

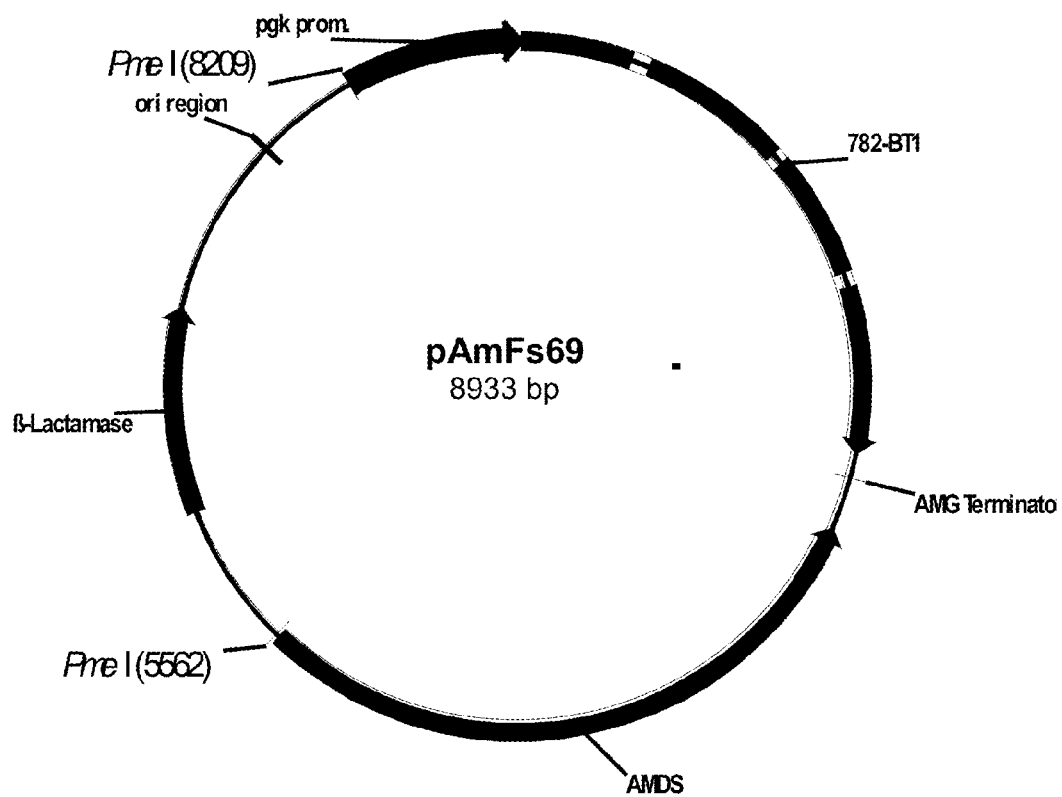


Fig. 2

M E S S A V Q E P T Q Q R S L R D R I F
1 ATGGAATCCA GCGCTGTACA GGAGCCGACT CAACAGCGCT CTTTGCGGGA TCGCATTTT
N L F R T S S S N D A P G L P A R L V T
61 AACCTCTTTC GTACCTCTTC CTCAAATGAT GCCCGGGTC TTCCGGCAAG ACTCGTAACC
A E S A A Q N E G S A L I Y P P R E P D
121 GCTGAGAGCG CAGCGCAAAA CGAAGGGTCG GCGTTAATCT ATCCGCCACG GGAGCCTGAT
A R T R L L E S Y D R G E R G L R N S G
181 GCAAGGACTC GTCTTCTCGA ATCGTACGAT CGCGGGGAAC GTGGTCTGAG GAACTCCGGC
V H G T F S S R P E Q E E I Q K W D A S
241 GTTCATGGGA CTTTTCTTC ACACCTGAA CAGGAAGAAA TCCAAAAATG GGATGCAAGC
S L Q N A G N E E R S Q S P G G A D G H
301 TCTTTGCAGA ATGCTGGTAA CGAAGAAAGA TCTCAGTCCC CAGGAGGAGC AGACGGCCAT
I G S P G D V S G Y P Q G P E N I P S L
361 ATTGGGTCTC CCGGCGACGT CTCAGGATAC CCACAGGGAC CAGAGAATAT ACCATCGCTA
D S S F T A L H M K N H K S L
421 GACTCCTCTT TCACAGCATT GCACATGAAG AATCATAAAT CTCTGTAGGT TTATAATCAC

481 GTTCGCCCTG CTTTCTAACA CAATTGTTAT CTCCATCGTG GAGACAACTA ACGTTTCATCA
Y I S Y Y I P F F N W I T Q Y R W S Y
541 AGGTATATAT CTTACTACAT CCCATTTTTC AATTGGATTA CTCATAACCG GTGGTCGTAC
I R G D L V A A T T I A S I Y I P M A L
601 ATTCGAGGTG ATTTGGTTGC TGCGACAACC ATTGCGTCCA TCTATATCCC TATGGCTTTG
S L S S N L A H A P P I N G L Y S F V I
661 TCCTTATCCT CAAATCTCGC CCACGCACCT CCTATCAATG GCCTCTACTC TTTTGTGATC
N P F I Y A I F G S S P L L I V G P E A
721 AACCCTTTCA TCTATGCGAT CTTCCGGGAGC AGCCCGCTGT TAATAGTGGG CCCAGAAGCA
A G S L L T G T I V K T S V R P G P S G
781 GCAGGCTCCT TGCTTACTGG CACGATTGTC AAAACTAGTG TCAGACCAGG CCCATCTGGT
E D D E V A N A I V V G I A T A M A G A
841 GAGGACGACG AAGTAGCGAA TGCCATCGTG GTCCGGCATAG CCACTGCAAT GGCGGGCGCC
M I L I A G L T R L G F L D N V L S R P
901 ATGATACTGA TCGCTGGGCT TACACGCTG GGATTTCTGG ACAATGTGCT GAGCCGGCCC
F L R G F I T A I G F V I F V D Q L I P
961 TTTCTTAGGG GTTTCATTAC AGCGATCGGT TTTGTGATTT TTGTGGATCA ACTCATCCCC
E V G L T E L A K E A G V T H G T T V D
1021 GAAGTCGGAT TGACCGAGCT AGCAAAGGAA GCTGGTGTTA CCCATGGGAC TACAGTTGAC
K L M F L I R N I G G C H A L T T A V A
1081 AAGCTCATGT TCCTTATAAG AAACATAGGA GGTGCGCATG CGCTTACAAC CGCGGTGGCT
F G S F A I I M V F R
1141 TTTGGGAGCT TTGCTATTAT AATGGTATTT CGGTTAGTGT TGGTGACTCG GAAGCCTGGT
T L K K M L Q P R Y P Q
1201 GCTTAGACTG ATTACCATTA CAGGACTCTC AAGAAAATGC TCCAGCCGCG GTATCCTCAG
V I Y L P D R I L V V I L S A V L T W H
1261 GTGATTTATC TTCCGGACCG AATTCTCGTA GTTATTCTTT CAGCCGTCCT GACATGGCAT
L G W D D K G L E I L G P L K Q N A N G
1321 CTTGGTTGGG ATGACAAAGG GTTGGAGATT CTTGGGCCCT TGAAACAAAA TGCCAATGGC
L F A F K W P F Q F S Q M K H V R A A M
1381 CTTTTTTCGT TCAAATGGCC TTTCCAGTTT AGCCAGATGA AGCATGTACG CGCTGCAATG
S T S F V I A L L G F F E S S V A A K G
1441 AGTACTTCTT TCGTCATCGC GTTACTTGGC TTTTTCGAGT CTTCTGTTGC CGCCAAGGGA
L S G E A R Q E G V Q G M P V S A N R E
1501 CTTAGTGGCG AGGCCAGACA AGAAGGTGTC CAGGGAATGC CTGTCACTGC TAACAGAGAG
M V A L G L A N T V G G C F M A L P A F
1561 ATGGTGGCGC TGGGTCTTGC TAATACTGTG GGGGGCTGTT TCATGGCGCT TCCTGCGTTT

Fig. 3A

G G Y A R S K V N A S T G A R S P M S S
1621 GGTGGCTATG CAAGAAGCAA AGTCAACGCT TCAACTGGAG CTCGGTCTCC GATGAGCAGC
I F L S I I T F V C I M V L L P Y L Y Y
1681 ATTTTCCTGA GCATTATTAC CTTGTTTGT ATCATGGTGC TTTTGCCGTA CTTATACTAT
L P
1741 CTTCCGGTGA GTCTCGACCC CAAATACTTC CGAGCGAAGG CTGAGAAAAT ATGTTGCAAT
K A V L S S M I S V V A F S L I E E
1801 AATTCAGAAA GCCGTTCTTT CTCTATGAT ATCTGTCGTC GCATTCAGTC TCATTGAAGA
C P H D V A F F I R L R G W T E L A L M
1861 ATGTCCTCAC GACGTGGCTT TCTTTATCCG ACTGCGCGGA TGGACGGAGC TAGCCCTAAT
L L I F V S T I F Y S L E L G I A L G I
1921 GCTTCTCATC TTTGTCTCGA CTATTTTCTA TTCTCTAGAG CTGGGAATTG CCCTTGGTAT
G L S I L I L I R H S T Q P R I Q I L G
1981 TGGCCTTTCT ATCTTGATCC TTATTCGCCA TTCTACGCAG CCTCGGATCC AAATTCTGGG
K I A G T T D R F D N A E L H P E S V E
2041 TAAGATAGCA GGCAC TACCG ACCGTTTTCG TAACGCTGAA CTCCACCCCG AGAGCGTTGA
L I E G A L I V K I P E P L T F A N T G
2101 GTTAATCGAA GGCGCGCTTA TTGTTAAGAT CCCGGAACCG CTCACCTTTG CCAATACTGG
E L K N R L R R L E L Y G S S R A H P S
2161 TGAGCTCAAG AATCGTCTTC GGCGGTTTGA ATTATATGGC AGTAGCCGAG CGCACCTTTC
L P P T R T P E H N K N I I F D V H G V
2221 TCTTCCCCC ACGCGCACCC CCGAACATAA CAAGAATATT ATATTGATG TTCATGGTGT
T S I D G S G T Q V L Y E I V D G Y A D
2281 TACTAGCATC GATGGTCCG GTACGCAAGT CTTATATGAG ATTGTGGACG GATATGCAGA
Q G V S V F F C R V A T R N V F R M F E
2341 CCAGGGGGTC AGCGTCTTCT TCTGCCGCGT CGCAACTCGC AATGTTTTCC GCATGTTTGA
R S G I V E R C G G I T H F V H G V D E
2401 ACGAAGTGGA ATTGTGGAAC GATGCGGTGG GATAACGCAC TTCGTTTCATG GTGTCGACGA
A L R L A E S E D E I E I *
2461 AGCCCTCCGC CTTGCCGAAT CGGAAGACGA GATTGAAATC TGA

Fig. 3B

M P G D L K T K I G H G A A K A L G I K
1 ATGCCGGGCG ATCTCAAAAC CAAAATTGGT CACGGCGCGG CCAAGGCCTT GGGGATCAAG
I P Y R D P L G V H A D P V T R G E S M
61 ATCCCTACC GTGATCCTCT CGGAGTTCAT GCTGACCCAG TCACACGAGG CGAGTCGATG
F S V G T I D T Y S Y L E P E P T P A E
121 TTCTCCGTCG GAACGATCGA CACATACTCC TATCTCGAGC CCGAACCAC TCCCGCTGAA
W L K E V C P S W H Q V G R Y F Y N L F
181 TGGCTGAAGG AAGTCTGCCC TAGCTGGCAT CAGGTGGGCC GTTATTTTCA CAACCTTTTC
P F L S W I T R Y N L Q W L L G D M I A
241 CCTTTCCTCT CGTGGATTAC GAGGTACAAC TTGCAATGGT TGCTGGGAGA TATGATTGCC

301 GGTAAGAGCC TTTCCACTGT GTTTGATTTG ATCGACAAGT AGACAACATA CTCATTGGAA
G V T V G A V V V P Q G M A Y A K L A
361 TGCAGCGTC ACGGTCGGTG CTGTGGTCGT TCCGCAGGGA ATGGCCTACG CTAACTGGC
N L P V E Y G L Y S S F M G V L I Y W F
421 AAACCTACCT GTAGAGTATG GTCTCTATTC CTCGTTTCATG GGTGTCTCTCA TTTATTGGTT
F A T S K D I T I G
481 TTTTGCCACC TCAAAGGATA TCACCATTGG TGTAAGTCAT TCTGCACCCA TGTGAGCATG
P V A V M S T L T
541 TATCTTGCTA ATATAGTATC TTCCCTGTTC AGCCGGTGGC TGTCTGTCT ACCCTTACAG
G K I V A E A Q T K L P D V E G H V I A
601 GTAAGATAGT TGCCGAGGCG CAAACGAAGC TCCCAGATGT CGAAGGGCAT GTAATCGCCT
S C L A I I C G A V V C A M G L L R L G
661 CCTGTTTGGC TATCATTTGT GGAGCCGTGG TTTGCGCTAT GGGCCTGCTT CGGCTGGGAT
F I V D F I P L P A I S A F M T G S A I
721 TTATCTGGA TTTCATTCTC CTGCCGGCAA TTTCAGCTTT CATGACGGGT TCCGCCATCA
N I C S G Q V K D M L G E T A D F S T K
781 ATATCTGCTC CGGACAGGTC AAAGACATGC TGGGAGAGAC GGCCGACTTC TCGACGAAAG
D S T Y L V I I N T L K H L P S A K I D
841 ATTCTACCTA TCTGGTTATC ATCAACACCC TCAAGCATCT TCCCTCCGCA AAAATCGATG
A A M G V S A L A M L Y I I R S G C N Y
901 CCGCCATGCT TGTCAGTGCT TTAGCTATGC TGTACATTAT CCGTTCGGGT TGCATTATG
G A K K F P R H A K V W F F V S T L R T
961 GCGCGAAGAA GTTCCCCCGT CATGCCAAGG TTTGGTTCTT CGTTTCGACT TTGCGCACAG
V F V I L F Y T M I S A A V N L H R R S
1021 TGTTCTGTGAT CTTGTTCTAT ACGATGATCA GTGCCGCTGT GAACTTGCAC CGGCGGTCTA
N P R F K L L G K V P R G F Q H A A V P
1081 ACCCGCGGTT CAAGCTCCTG GGTAAAGTTC CTCGTGGTTT CCAACATGCG GCTGTCCCTC
Q V N S R I I S A F A S E L P A S I I V
1141 AGGTAAATTC GAGGATCATC AGCGCATTTG CTAGCGAACT TCCTGCTTCG ATTATTGTCC
L L I E H I A I S K S F G R V N N Y T I
1201 TGCTTATCGA ACACATCGCT ATCTCGAAAT CCTTTGGCCG TGTCAACAAC TACACAATTG
D P S Q E L V A I G V S N L L G P F L G
1261 ATCCCTCTCA GGAGCTGGTT GCTATTGGTG TGTGCAACTT GCTTGGACCG TTCCTTGGTG
G Y P A T G S F S R T A I K S K A G V R
1321 GTTACCCAGC GACTGGATCG TTCTCCCGAA CTGCAATCAA ATCGAAAGCG GGTGTCCGCA
T P L A G V I T A V V V L L A I Y A L P
1381 CCCCCTTGC CGGTGTTATT ACTGCGGTTG TTGTCCTCCT CGCCATTAC GCTCTGCCCC
A V F F Y I P K A S L A G V I I H A V G
1441 CTGTCTTCTT TTACATCCCG AAAGCTTCCC TTGCTGGTGT CATCATTCAT GCAGTCGGTG
D L I T P P N T V Y Q F W R V S P L D A
1501 ACCTCATTAC CCCACCAAAC ACCGTTTACC AGTTCTGGCG CGTGTCCCCT CTGGATGCGA
I I F F I G V I V T V F T T I E I G I Y
1561 TCATTTTCTT TATCGGTGTT ATCGTGACTG TCTTCACCAC GATTGAGATC GGCATTACT
C T V C V S V A I L L F R V A K A R G Q
1621 GTACCGTTTG TGTGCTGTG GCCATTCTGC TGTTCGCGT CGCCAAGGCC CGCGGTCAAT

Fig. 4A

F L G R V T I H S V I G D H L V Q D D G
1741 TCTTAGGAAG AGTCACTATC CACTCGGTGA TCGGTGACCA TCTGGTACAG GATGATGGGA
K Y G S A N S P N A A S D D K D E L S R
1801 AATATGGGTC TGCCAACCTC CCTAATGCTG CCAGCGATGA CAAAGATGAA TTGAGCCGGT
S I F L P I N H T D G S N P D V E V Q Q
1861 CTATCTTCTT GCCTATCAAC CACACGGACG GATCGAATCC CGATGTCGAG GTGCAGCAAC
P Y P G I F I Y R F S E G F N Y P N A N
1921 CTTATCCTGG TATCTTCATC TACCGATTCT CGGAAGGATT CAACTACCCC AATGCCAATC
H Y T D Y L V Q T I F K H T R R T N P F
1981 ACTACACCGA TTATTGGTC CAGACTATCT TCAAGCATAC ACGTCGCACA AATCCGTTCT
S Y G K P G D R P W N N P G P R R G K S
2041 CCTACGGTAA ACCGGGTGAT CGGCCATGGA ATAATCCTGG CCCTCGCAGG GGCAAGTCTG
E D D E S H L P L L Q A V I L D F S S V
2101 AAGATGACGA GTCGCATTTG CCCTTACTGC AGGCTGTCTAT TCTTGACTTC TCATCCGTCA
N N V D V T S V Q N L I D V R N Q L D L
2161 ACAATGTTGA TGTGACCTCG GTCCAGAACC TCATCGATGT CCGCAATCAA CTCGACCTCT
Y A S P K T V Q W H F A H I N N R W T K
2221 ACGCTTCGCC TAAGACTGTG CAGTGGCACT TTGCTCATAT TAACAACCGC TGGACGAAAC
R A L A A A G F G F P S P D S D E G F Q
2281 GAGCCCTTGC AGCAGCAGGT TTCGGCTTCC CATCTCCGGA CTCGGATGAA GGATTCCAGA
R W K P I F S V A E I E G S A S A A A H
2341 GATGGAAGCC AATTTTCAGC GTGGCTGAGA TCGAAGGCAG TGCCTCTGCC GCAGCTCATG
A E M V N N R H T Q H N I K S E D L E H
2401 CAGAGATGGT GAACAACAGA CACACCCAGC ATAACATCAA GAGCGAAGAC CTCGAGCATG
G L K H D S E T T E R E T H G I E E S S
2461 GCCTCAAGCA CGATTTCAGAG ACCACCGAGC GTGAGACACA CGGCATCGAA GAATCCTCCG
D A S S T R E D K L Q R D L K D S K A Y
2521 ATGCCAGCAG CACCCGGGAG GACAAGTTGC AACGGGACCT GAAGGATAGC AAGGCTTACC
R S R R R V A M V Q G L N R P F F H I D
2581 GCAGTCGCCG AAGGGTCGCT ATGGTGCAGG GCCTCAACCG GCCATTCTTC CACATCGACC
L T S A L Q S A L A N A G E Q P D P K M
2641 TGACTAGTGC ACTGCAGAGT GCCTTGGCCA ACGCGGGCGA GCAGCCGGAC CCTAAAATGA
N V L D A *
2701 ATGTCCTTGA TGCATAG

Fig. 4B

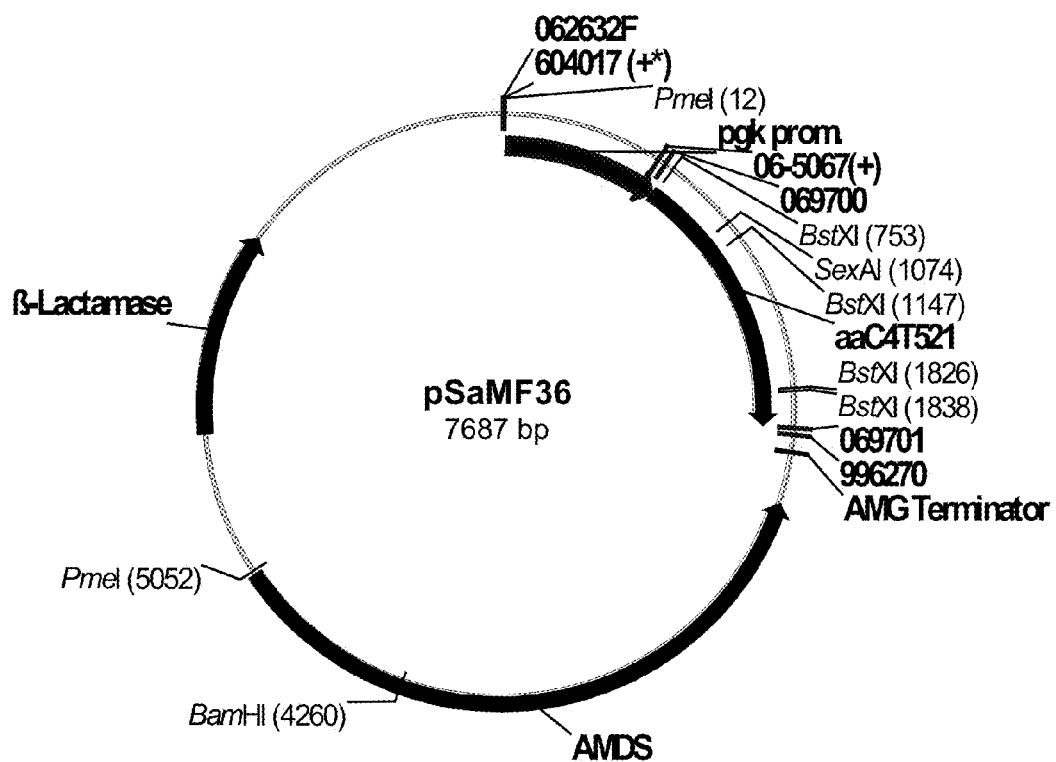


Fig. 5

M H D H S T G S S P Y I S D V E T L N H
1 ATGCACGACC ACAGCACTGG ATCTAGTCCA TACATCTCGG ACGTGGAAC CTTGAACCAC
A C E K S V N P E T K V S Q P Q E S P I
61 GCCTGCGAGA AGTCCGTCAA CCCCAGAGACC AAAGTCTCCC AGCCTCAGGA ATCTCCCAT
I S N N E H Q E F V K L G I R Q R L R H
121 ATCAGCAATA ATGAACATCA GGAGTTTGTT AAGCTGGGCA TCCGCCAACG GCTGCGTCAT
F T W A W Y T L T M S A G G L A L L L R
181 TTCACCTGGG CCTGGTATAC CCTAACCATG AGCGCAGGTG GACTGGCCCT TCTTCTCCGC
N Q P Y Q F K G L K E I G L V V Y I A N
241 AACCAGCCGT ATCAATTCAA GGGGTTGAAG GAGATAGGCC TGGTGGTATA CATAGCCAAT
L V F F T I I G S L M I T R F V L Y N N
301 CTCGCTCTCT TTACTATCAT CGGCTCTCTT ATGATCACCA GGTTTGTTCT TTACAACAAC
L M D S L R H D R E G F F F P T F W L S
361 CTGATGGACT CTCTCCGCCA CGACCGAGAA GGTTTCTTCT TTCCAACCTT CTGGCTCTCC
I A T M I S G L S A Y F S T E D T H R L
421 ATCGCCACCA TGATTAGTGG TCTATCTGCC TACTTCTCTA CTGAAGACAC GCACCGCCTC
N Y A L E G L F W A Y C I F T F A S A V
481 AATTATGCTC TCGAGGGTCT CTTCTGGGCG TACTGTATCT TCACGTTTGC CTCAGCAGTG
I Q Y S F V F S Y H T F P L Q T M M P S
541 ATCCAGTACT CTTTGTCTT CTCCTATCAC ACGTTCCCTC TGCAAACTAT GATGCCATCA
W I L P A F P I M L S G T I A S A S S
601 TGGATCTTAC CGGCATTCCC TATCATGCTG AGCGGAACCA TTGCCTCTGC CGCTTCCAGC
Y Q P A V S A T P M I V A G I T F Q G L
661 TACCAGCTTG CGGTGTCTGC CAGGCCTATG ATTGTTGCCG GCATCACGTT CCAGGGACTC
G F C I S F M M Y A H Y I G R L M E T G
721 GGATTCTGCA TCAGCTTCAT GATGTACGCC CACTACATCG GGCGTCTGAT GGAGACGGGC
I P S S E H R P G M F I C V G P P A F T
781 ATCCCTTCGA GCGAGACCG TCCTGGTATG TTCATCTGTG TCGGCCCCC TGCCTTCACG
L L A I I G M A N G L P E G F S I L G D
841 CTGCTGGCTA TCATCGGCAT GGCCAACGGC CTTCCCGAGG GCTTCAGTAT CCTGGGCGAT
G G M D D R H I M R V L A V C A G M F L
901 GGTGGCATGG ACGACCGTCA CATCATGCGA GTACTGGCCG TCTGCGCGGG CATGTTCCCTC
W A L S I W F F C V A L G S V V R A P P
961 TGGGCTCTGA GCATTGTTT CTTCTGTGTC GCTCTGGGCT CAGTTGTGCG GGCGCCTCCC
H D F H L N W W A M V F P N T G L T L A
1021 CATGATTTC ACCTCAACTG GTGGGCTATG GTCTTCCCTA ACACCGGACT CACTCTCGCC
T I T L A K S L D S A A L K W V G V G M
1081 ACCATCACCC TGGCCAAGTC ACTGGACAGT CCCGCGTTGA AATGGGTGGC CGTGGGCATG
S L C V I C M F I F V F V S T I R A V L
1141 TCCCTCTGCG TGATCTGCAT GTTCATCTTC GTCTTCGTGA GCACCATTAG GGCTGTTCTC
L K R I M W P G R D E D V S E L F E *
1201 TTGAAGAGGA TCAATGTGGC AGGTCGGGAT GAGGATGTGT CCGAGTTGTT CGAATGA

Fig. 6

M V K A
1 ATGGTCAAAG CTGGTGAGTT AGCAATCCTT AACAGATGAC ACTCTCATAG GTACTAACTC
A V L G A S G G I G Q
61 GAAACGTTAG CCGTACTTGG AGCTTCTGGT GGCATTGGCC AGGTATGGAT ATCCCCACGC
P L S
121 CTTACAACCC TGGTCACAAT ATGACCTTGT TCGATACTGA CTATCTCCCA AGCCACTGTC
L L L K T C P L V E E L A L Y D V V N T
181 TCTCCTGTTG AAGACCTGTC CCTTAGTTGA AGAGCTTGCT CTCTACGATG TTGTGAACAC
P G V A A D L S H I S S I A
241 CCCTGGTGTT GCTGCTGATC TATCCACAT CTCGTCTATC GCTGTACGTT ACTGCCACAA
K
301 TGCGAATTGC CCGATGGAAG AGGCGAAAAA TGGTATCTTG CTTACCTGGG CGATTAGAAA
I S G F L P K D D G L K Q A L T G A N I
361 ATCTCTGGTT TTCTGCCCAA AGATGATGGG CTGAAGCAGG CCCTTACTGG TGCTAATATT
V V I P A G I P
421 GTTGTCTATC CCGCTGGTAT TCCCCGTAAG TCCCTACCCT TTGCGATTGC TCCTCGTATG
R K P G M T R D D
481 TTCGCTGGTG GCCAGTTTTC TGATAGTTGA TAGGCAAGCC TGGTATGACC CGTGACGACC
L F K I N A G I V R D L V K G I A E F C
541 TCTTCAAGAT CAACGCCGGC ATAGTGCAGG ACTTGGTCAA GGGTATCGCC GAGTTCTGCC
P K A F V L V I S N P V N S T V P I A A
601 CCAAGGCCTT TGTTCTGGTT ATCTCAAACC CCGTTAATTC TACTGTTTCCT ATTGCTGCAG
E V L K A A G V F D P K R L F G V T T L
661 AGGTGCTCAA AGCCGCTGGC GTCTTTGACC CGAAGCGCCT CTTTGGTGTC ACCCACTGG
D V V R A E T F T Q E F S G Q K D P S A
721 ACGTCGTTTC TGCAGAGACT TTCACCCAAG AGTTCTCGGG CCAGAAGGAT CCTTCTGCTG
V Q I P V V G G H S G E T I V P L F S K
781 TTCAAATCCC AGTTGTTGGT GGCCACTCTG GAGAGACCAT TGTCCCCCTC TTCAGCAAGA
T T P A I Q I P E E K Y D A L I H
841 CTACCCCCGC AATTCAGATA CCCGAGGAGA AGTATGACGC ACTGATCCAC CGTAGGTTGT
R V Q F
901 CCCAAAGAAT CTCATGAATA TCTTGCTGTA AGCACTAACT ATGCTTCAGG CGTCCAATTT
G G D E V V Q A K D G A G S A T L S M A
961 GGTGGAGATG AGGTGGTCCA AGCTAAGGAC GGTGCTGGTT CCGCCACCTT GTCTATGGCC
Y A G Y R
1021 TATGCCGGTT ACAGGTAGGG ATGCTGCGTA CCGTGAGAGC ACTCGCGGCT AACATGCCAT
F A E S V I K A S K G Q T G I V E P T
1081 AGGTTCGCTG AGAGTGTAAT CAAAGCTTCA AAGGGTCAA CGGGTATTGT CGAGCCTACC
F V Y L P G I P G G D E I V K A T G V E
1141 TTCGTCTACC TGCCTGGAAT TCCCGGCGGT GATGAGATCG TTAAGGCAAC TGGCGTGGAA
F F S T L V T L G
1201 TTCTTCTCTA CTCTTGTAAC CTTAGGAGTA AGATTCATCT CCTCACAGAA TCTTCGTTCA
T N G A E K A S N V
1261 TATCACGCCA GGCTAACGCT ATTAAACAGA CTAATGGCGC AGAGAAGGCT AGCAACGTTT
L E G V T E K E K K L L E A C T K G L K
1321 TTGAGGGCGT GACCGAGAAG GAAAAGAAGC TTCTCGAGGC TTGCACGAAA GGCCTTAAGG
G N I E K G I D F V K N P P P K *
1381 GTAATATCGA GAAAGGCATC GACTTCGTGA AGAACCACC ACCAAAGTAA

Fig. 7

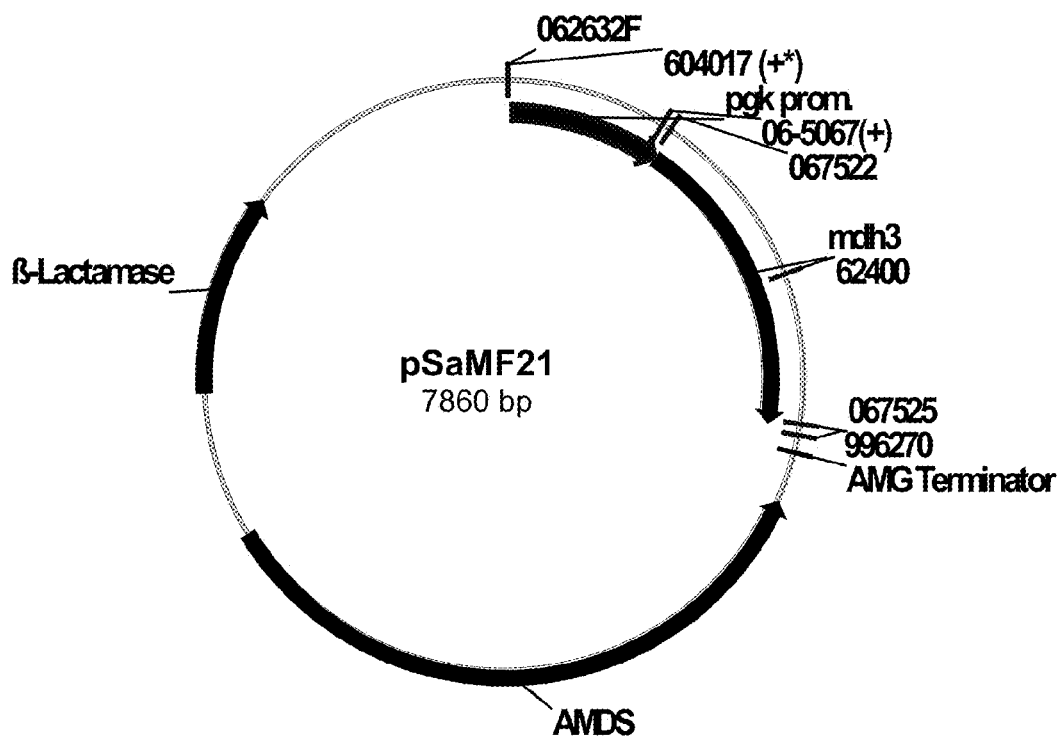


Fig. 8

M A A P F R Q P E E A V D D T E F I D D
1 ATGGCGGCTC CGTTTCGTCA GCCTGAGGAG GCGGTCGATG ACACCGAGTT CATCGATGAC
H H E H L R D T V H H R L R A N S S I M
61 CACCATGAAC ACCTCCGTGA TACCGTGCAC CATCGGTTGC GCGCAATTC CTCCATTATG
H F Q K I L V A N R G E I P I R I F R T
121 CACTTCCAGA AGATCCTCGT CGCCAACCGT GGTGAGATCC CCATTCGTAT CTTCAGAACG
A H E L S L Q T V A I Y S H E D R L S M
181 GCCCAGGAGC TGTCTTGCA GACGGTTGCT ATCTACTCTC ATGAGGATCG ACTGTCAATG
H R Q K A D E A Y M I G H R G Q Y T P V
241 CACCGTCAAA AGGCCGATGA GGCCTACATG ATTGGCCACC GCGGTCAGTA CACCCCTGTC
G A Y L A G D E I I K I A L E H G V Q L
301 GGTGCGTACC TGGCGGGCGA TGAGATCATC AAGATCGCCC TGGAGCACGG TGTCCAGCTG
I H P G Y G F L S E N A D F A R K V E N
361 ATCCACCCGG GCTACGGTTT CTTGTCCGAG AACGCCGACT TCGCCCGCAA GGTGAGAAC
A G I V F V G P T P D T I D S L G D K V
421 GCCGCGATG TCTTTGTGGG ACCCACTCCC GATACCATTG ACAGTTGGG TGACAAGGTG
S A R R L A I K C E V P V V P G T E G P
481 TCGGCCCGTC GGCTGGCCAT TAAGTGCGAG GTCCCTGTCG TTCCGGGTAC GGAGGGCCCC
V E R Y E E V K A F T D T Y G F P I I I
541 GTCGAGCGCT ATGAGGAGGT CAAGGCGTTC ACAGACACCT ATGGCTTCCC CATCATCATC
K A A F G G G G R G M R V V R D Q A E L
601 AAGCTGCGCT TTGGCGGTGG TGGCGGTGGT ATGCGTGTGG TCCGTGACCA GGCGGAGCTG
R D S F E R A T S E A R S A F G N G T V
661 CGTGACTCGT TCGAGCGAGC CACCTCTGAG GCCCGCTCCG COTTCCGCAA TGGTACCCTG
F V E R F L D K P R H I E V Q L L G D S
721 TTCGTCGAGC GCTTCTCGA CAAACCCAAAG CACATTGAAG TCCAGCTTCT GGTGACAGC
H G N V V H L F E R D C S V Q R R H Q K
781 CACGGCAACG TTGTCCATCT GTTTGAGCGT GACTGCTCCG TGCAGCGTCG TCACCAGAAG
V V E V A P A K D L P A D V R D R I L A
841 GTCGTTGAGG TTGCTCCGGC TAAGGACCTG CCAGCCGATG TCCGGGACCG CATCCTGGCC
D A V K L A K S V N Y R N A G T A E F L
901 GATGCTGTGA AGCTGGCCAA GTCCGTCAAC TACCGTAACG CCGGTACAGC TGAGTTCCTG
V D Q Q N R H Y F I E I N P R I Q V E H
961 GTGGACCAGC AGAACCGCCA CTACTTCATT GAAATCAATC CTCGTATCCA AGTCGAGCAC
T I T E E I T G I D I V A A Q I Q I A A
1021 ACCATCACCG AAGAGATTAC TGGTATCGAT ATCGTGGCTG CACAGATCCA GATTGCTGCT
G A S L E Q L G L T Q D R I S A R G F A
1081 GGTGCAAGCC TCGAGCAACT GGGCCTGACT CAGGACCGCA TCTCCGCCCG CGGATTTGCC
I Q C R I T T E D P A K G F S P D T G K
1141 ATTCAATGTC GTATCACCAC GGAAGATCCC GCCAAGGGGT TCTCTCCGGA TACTGGTAAG
I E V Y R S A G G N G V R L D G G N G F
1201 ATTGAGGTTT ATCGTTCCGC TGGTGGTAAC GGTGTCCGTC TGGATGGTGG TAACGGTTTC
A G A I I T P H Y D S M L V K C T C R G
1261 GCTGGTGCTA TCATCACCCC TCACTACGAC TCCATGCTGG TCAAGTGAC C TGCCGTGGT
S T Y E I A R R K V V R A L V E F R I R
1321 TCGACCTATG AAATCGCTCG TCGCAAGGTT GTGCGTGCCT TGGTCGAGTT CCGTATTCTG
G V K T N I P F L T S L L S H P T F V D
1381 GGTGTGAAGA CCAACATTCC CTTCTGACT TCGCTTCTGA GCCACCCGAC CTTCTGTCGAT
G N C W T T F I D D T P E L F S L V G S
1441 GGAAGTCTGT GGACCACTTT CATCGACGAC ACCCCTGAAT TGTCTCTCT TGTCCGGCAGT
Q N R A Q K L L A Y L G D V A V N G S S
1501 CAGAACCGTG CCCAGAAGCT GCTCGCATA C TC G G C G A T G T A G C T G T C A A C G T A G C
I K G Q I G E P K L K G D V I K P K L F
1561 ATCAAGGGCC AAATGGCGA GCCCAAGCTC AAGGGTGATG TCATCAAGCC GAAGCTTTTC
D A E G K P L D V S A P C T K G W K Q I
1621 GATGCCGAGG GCAAGCCGCT TGACGTTTCC GCCCCTGCA CCAAGGGTTG GAAGCAGATT
L D R E G P A A F A K A V R A N K G C L
1681 CTGGACCGGG AGGGTCCGGC TGCCTTTGCG AAGGCCGTGC GTGCCAACAA GGGTTGCTTG
I M D T T W R D A H Q S L L A T R V R T
1741 ATCATGGATA CTACCTGGCG TGACGCCAC CAGTCTTTGC TGGCCACCCG TGTGCGTACC
I D L L N I A H E T S Y A Y S N A Y S L
1801 ATCGACTTGT TGAACATCGC CCATGAGACC AGCTACGCCT ACTCCAATGC GTACAGTTTG

Fig. 9A

1861 E C W G G A T F D V A M R F L Y E D P W
GAATGCTGGG GTGGTGCTAC CTTGCGATGTG GCCATGCGTT TCCTCTATGA GGACCCCTGG
D R L R K M R K A V P N I P F Q M L L R
1921 GACCGCTGCG GCAAGATGCG TAAGGCTGTT CCTAACATCC CATTCCAGAT GTTGCTCCGT
G A N G V A Y S S L P D N A I Y H F C K
1981 GGTGCCAACG GTGTGCGCTA CTCTTCCCTC CCAGACAACG CCATCTACCA CTTCTGTAAG
Q A K K C G V D I F R V F D A L N D V D
2041 CAGGCTAAGA AGTGCGGTGT CGACATTTTC CGTGTTCGTCG ACGCCCTCAA CGATGTCGAT
Q L E V G I K A V H A A E G V V E A T M
2101 CAGCTCGAGG TCGGTATCAA GGCTGTTCAT GCTGCCGAGG GTGTTGTCGA GGCCACCATG
C Y S G D M L N P H K K Y N L E Y Y M A
2161 TGCTACAGCG GTGACATGCT GAACCCCCAC AAGAAGTACA ACCTGGAGTA CTACATGGCC
L V D K I V A M K P H I L G I K D M A G
2221 TTGGTGGATA AGATTGTAGC CATGAAGCCT CACATCCTTG GTATCAAGGA TATGGCCGGT
V L K P Q A A R L L V G S I R Q R Y P D
2281 GTGCTGAAGC CCCAGGCCGC TCGCTGTGTC GTGGGCTCCA TCCGTCAGCG CTACCCTGAC
L P I H V H T H D S A G T G V A S M I A
2341 CTTCCTCATCC ACGTCCACAC CCACGACTCC GCTGGTACTG GTGTAGCTTC CATGATTGCC
C A Q A G A D A V D A A T D S M S G M T
2401 TGTGCCCAGG CGGGTGCCGA CGCCGTGGAC GCCGCGACCG ACAGCATGTC CGGTATGACC
S Q P S I G A I L A S L E G T E Q D P G
2461 TCCCAGCCTA GCATTGGTGC CATTCTGGCC TCTCTTGAGG GCACTGAGCA AGACCCCGGT
L N L A H V R A I D S Y W A Q L R L L Y
2521 CTCAACCTCG CCCACGTGCG CGCTATTGAT AGCTACTGGG CACAGCTGCG CTTGCTCTAC
S P F E A G L T G P D P E V Y E H E I P
2581 TCTCCTTTCG AGGCGGGTCT CACTGGCCCC GACCCTGAGG TCTACGAGCA CGAGATCCCT
G G Q L T N L I F Q A S Q L G L G Q Q W
2641 GGTGGTCAGT TGACCAACCT TATCTTCCAG GCCAGTCAGC TCGGCTTGGG CCAGCAGTGG
A E T K K A Y E A A N D L L G D I V K V
2701 GCCGAACCA AGAAGGCCTA TGAGGCGGGT AATGATTTAC TCGGCGACAT TGTAAGGGT
T P T S K V V G D L A Q F M V S N K L T
2761 ACTCCACCT CCAAGGTGGT CGGTGACTTG GCTCAGTTCA TGGTCTCGAA CAAACTGACT
P E D V V E R A G E L D F P G S V L E F
2821 CCAGAGGATG TTGTTGAGCG TGCTGGTGAG CTGGACTTCC CTGGTTCTGT GCTCGAATTC
L E G L M G Q P F G G F P E P L R S R A
2881 CTCGAAGGTC TCATGGGACA GCCCTTCGGT GGATTCCCCG AGCCATTGCG CTCCCAGGCC
L R D R R K L E K R P G L Y L E P L D L
2941 CTGCGCGATC CGCGCAAGCT CGAGAAGCGT CCAGGTCTCT ACCTCGAGCC TTTGGATTTG
A K I K S Q I R E K F G A A T E Y D V A
3001 GCTAAGATCA AGAGCCAGAT CCGTGAGAAG TTCGGTGCTG CTAAGTGAAG TGACGTGGCC
S Y A M Y P K V F E D Y K K F V Q K F G
3061 AGCTATGCCA TGATATCCCAA GGTCTTCGAG GACTACAAGA AGTTCTGTTCA GAAGTTCGGT
D L S V L P T R Y F L A K P E I G E E F
3121 GATCTCTCCG TCTTGCCAC ACGGTACTTC TTGGCCAAGC CTGAGATTGG CGAGGAGTTC
H V E L E K G K V L I L K L L A I G P L
3181 CACGTTGAGC TGGAGAAGGG TAAGGTGCTC ATCCTGAAGT TGTGCGCAT CGGCCCTCTT
S E Q T G Q R E V F Y E V N G E V R Q V
3241 TCAGAGCAGA CTGGTCAGCG TGAGGTCTTC TACGAAGTCA ACGGTGAGGT GCGCCAGGTC
A V D D N K A S V D N T S R P K A D V G
3301 GCTGTTGATG ACAACAAGGC TTCCGTGGAC AACACTTCAC GCCCTAAGGC CGATGTGGGT
D S S Q V G A P M S G V V V E I R V H D
3361 GACAGCAGCC AGGTGCGTGC TCCTATGAGC GGTGTGGTTG TTGAAATCCG TGTCCACGAT
G L E V K K G D P L A V L S A M K M
3421 GGTCTGGAGG TTAAGAAGGG TGACCCACTT GCCGTCTGA GTGCCATGAA GATGGTAAGT
E M
3481 TCATTCCGAA TCATTTTCT CACTGGTCAA CTACAGATGC TAACAGCTTA TCCAGGAAAT
V I S A P H S G K V S S L L V K E G D S
3541 GGTATCTCT GCTCTCACA GTGGAAAGGT CTCCAGCTTG CTGGTCAAGG AGGGCGATTG
V D G Q D L V C K I V K A *
3601 TGTGGATGGC CAGGATCTCG TCTGCAAGAT CGTCAAAGCG TAA

Fig. 9B

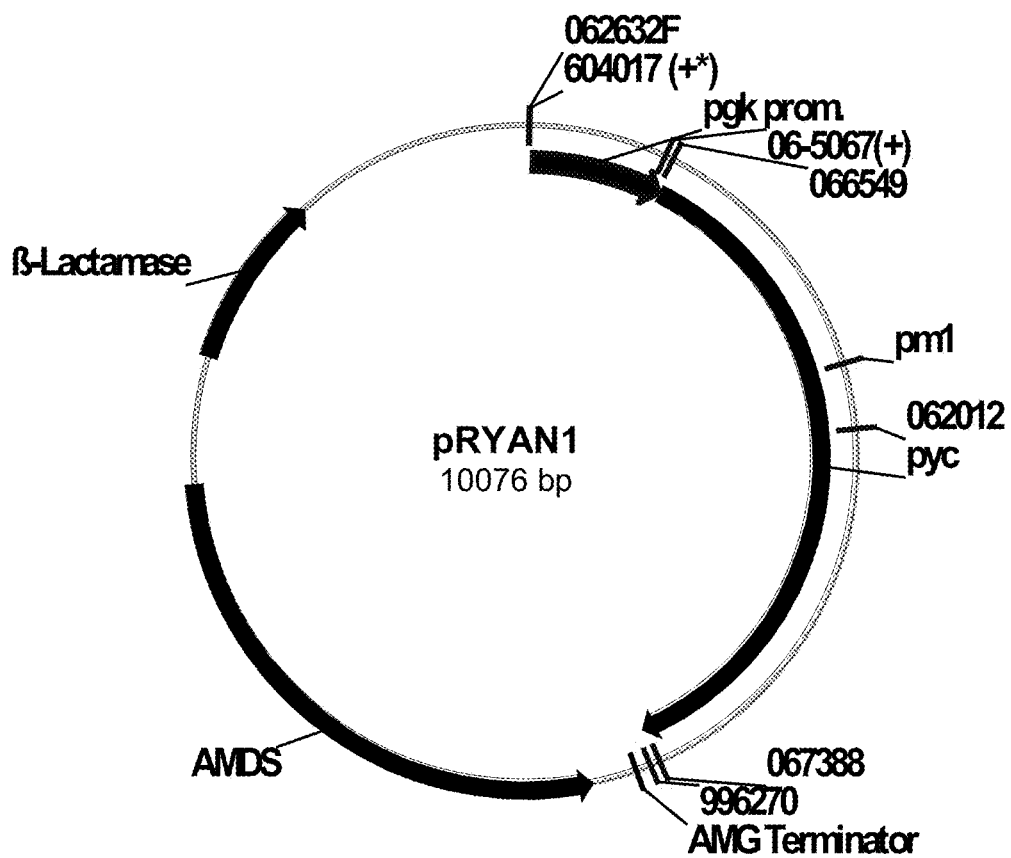


Fig. 10

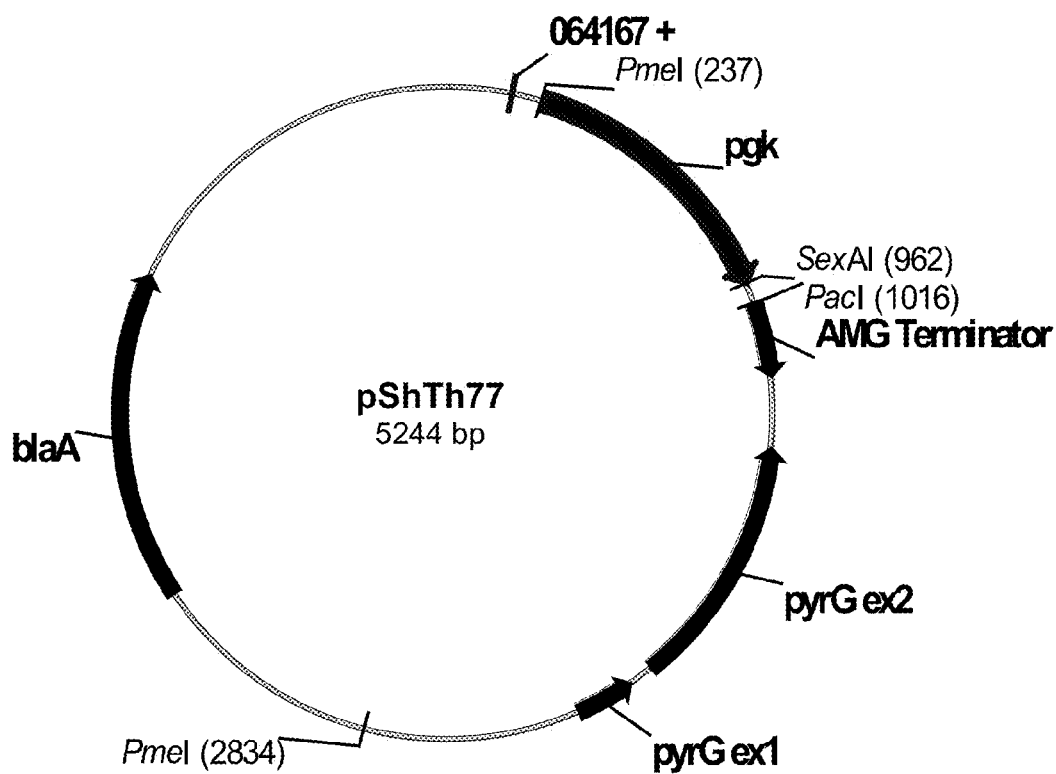


Fig. 11

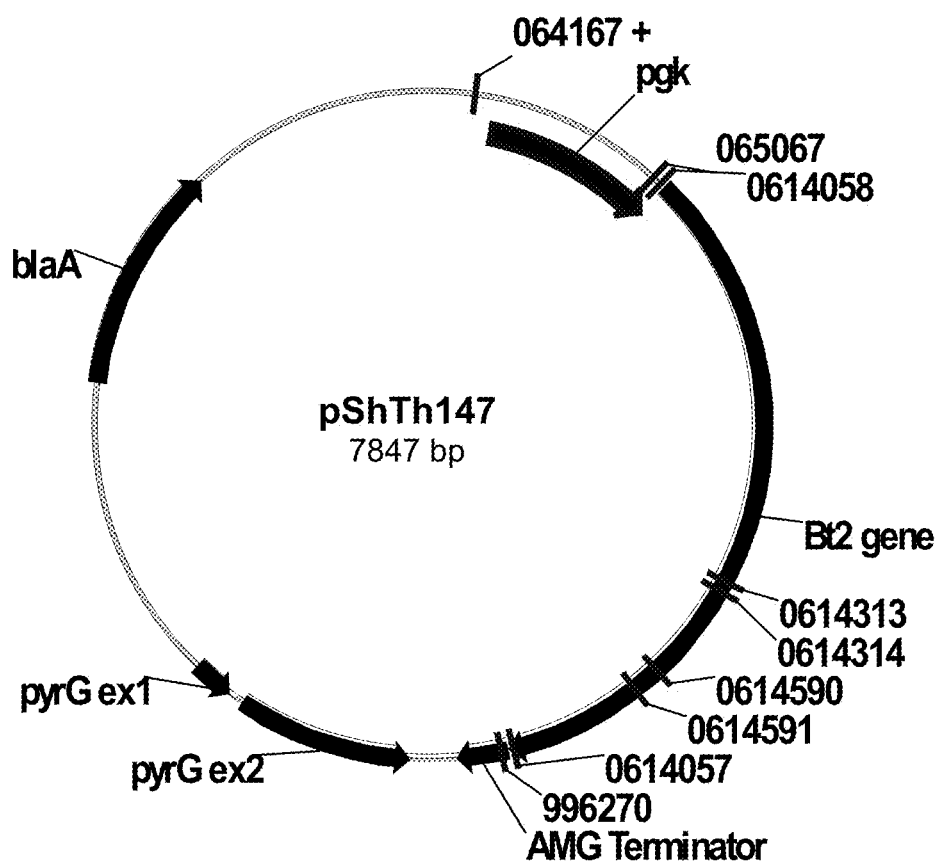


Fig. 12

MICROORGANISMS FOR C4-DICARBOXYLIC ACID PRODUCTION

CROSS REFERENCE TO RELATED APPLICATIONS

This application is a divisional of U.S. patent application Ser. No. 13/407,584, filed Feb. 28, 2012, now U.S. Pat. No. 8,722,387, which claims priority benefit of U.S. Provisional Application No. 61/447,286, filed Feb. 28, 2011. The content of these applications are fully incorporated herein by reference.

REFERENCE TO A SEQUENCE LISTING

This application contains a Sequence Listing in computer readable form, which is incorporated herein by reference.

BACKGROUND OF THE INVENTION

1. Field of the Invention

The present invention relates to methods for the recombinant production of C4-dicarboxylic acids (e.g., malic acid).

2. Description of the Related Art

Organic acids have a long history of commercial use in a variety of industries. For example, organic acids are used in the food and feed industries (citric acid, ascorbic acid, lactic acid, acetic acid, and gluconic acid) as monomers for the production of various polymers (adipic acid, lactic acid, acrylic acid, and itaconic acid), as metal chelators (gluconic acid), and as “green” solvents (acetic acid) (Sauer et al., 2008, *Trends in Biotechnology* 26: 100-108). Organic acids may themselves be commercial products or they may be chemical building blocks used in the manufacture of other chemicals. In addition to specialty applications, it has long been recognized that C4-dicarboxylic acids can also serve as building block compounds for the production of large volume industrial chemicals, such as 1,4-butanediol, tetrahydrofuran, and gamma-butyrolactone. The cost of producing these large volume industrial chemicals by traditional petrochemical routes has increased significantly due to the high cost of petroleum derived building blocks.

Organic acids may be produced commercially either by chemical synthesis from petroleum derived feedstocks (e.g., fumaric acid, malic acid, acrylic acid, and adipic acid) or by microbial fermentation (e.g., citric acid, lactic acid, gluconic acid, and itaconic acid). Some organic acids—such as fumaric acid and malic acid—can also be produced by microbial fermentation, but are currently produced commercially by chemical synthesis from petrochemical feedstocks due to lower production costs. However, the rising cost of petroleum derived building block chemicals, the geopolitical instability affecting crude oil prices, and the desire to implement manufacturing processes that utilize feedstocks derived from renewable resources have stimulated a renewed interest in producing organic acids and other chemicals by microbial fermentation.

While C4-dicarboxylic acids such as malic acid are produced commercially today by chemical synthesis from petrochemical sources, it can also be produced by microbial fermentation. Malic acid has been produced at high levels in genetically engineered yeast (*Saccharomyces cerevisiae*) (Zelle et al., 2008, *Appl. Environ. Microbiol.* 74: 2766-2777) and naturally occurring filamentous fungi such as *Aspergillus* spp. (U.S. Pat. No. 3,063,910; Bercovitz et al., 1990, *Appl. Environ. Microbiol.* 56: 1594-1597). Abe et al. (U.S.

Pat. No. 3,063,910) and Bercovitz et al. (1990, *Appl. Environ. Microbiol.* 56: 1594-1597) reported high levels of malic acid production in several species of *Aspergillus*. Moreover, Battat et al. (1991, *Biotechnol. Bioengineering*, 37: 1108-1116) reported malic acid production as high as 113 g/L by *Aspergillus flavus* in a stirred fermentor under optimized conditions. Dicarboxylic acid production by microbial fermentation in yeast is described in WO 2010/003728. Malic acid production by microbial fermentation is also described in WO 2009/011974, WO 2009/155382 and WO2010/111344. Improvement of the production of C4-dicarboxylic acids such as malic acid by genetic engineering may enable economical commercial malic acid production by fermentation.

Malic acid overproduction in a host such as *Aspergillus* spp. occurs under specific culture conditions (aerobic conditions and high C:N ratio; calcium carbonate may also be added as a neutralizing agent and as source of CO₂ for malic acid biosynthesis). Under these conditions, overflow metabolism via the cytosolic, reductive tricarboxylic acid (TCA) cycle results in increased malic acid biosynthesis and secretion into the culture medium. Increased malic acid production has been reported in *Saccharomyces cerevisiae* by increasing the level of pyruvate carboxylase (Bauer et al., 1999, *FEMS Microbiol. Lett.* 179: 107-113) or malate dehydrogenase (Pines et al., 1997, *Appl. Microbiol. Biotechnol.* 48: 248-255) using genetic engineering and increasing expression of a malic acid transporter (Zelle et al., 2008, *supra*). It has been suggested, based on biochemical evidence, that malate dehydrogenase activity is limiting malic acid production in *Aspergillus flavus* strain ATCC 13697 (Peleg et al., 1988, *Appl. Microbiol. Biotechnol.* 28: 69-75). U.S. application Ser. No. 12/870,523, entitled “Methods for Improving Malic Acid Production in Filamentous Fungi” filed Aug. 27, 2010, and U.S. Provisional application No. 61/356,868, entitled “Polypeptides Having C4-dicarboxylic acid Transporter Activity and Polynucleotides Encoding Same” filed Jun. 21, 2010—the contents of which are hereby incorporated by reference in their entireties—describe C4-dicarboxylic acid production.

It would be advantageous in the art to improve C4-dicarboxylic acid production, such as malic acid production, as a result of genetic engineering using recombinant DNA techniques. The present invention provides, inter alia, methods for improving C4-dicarboxylic acid production (e.g., malic acid production).

SUMMARY OF THE INVENTION

The present invention relates to recombinant host cells comprising bicarbonate transporter activity, wherein the host cell produces (or is capable of producing) an increased amount of a C4-dicarboxylic acid (e.g., malic acid). In one aspect, the recombinant host cells comprise a heterologous polynucleotide encoding a bicarbonate transporter (e.g., a sulfate-bicarbonate transporter), wherein the host cell produces (or is capable of producing) and/or secretes (or is capable of secreting) a greater amount of a C4-dicarboxylic acid (e.g., malic acid) compared to the host cell without the heterologous polynucleotide when cultivated under the same conditions. In some aspects, the host cell further comprises a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter, a heterologous polynucleotide encoding a malate dehydrogenase, and/or a heterologous polynucleotide encoding a pyruvate carboxylase. In some aspects, the host cell is a filamentous fungal host cell, such as an *Aspergillus oryzae* host cell.

The present invention also relates to methods of using recombinant host cells for the production of a C4-dicarboxylic acid. In one aspect, the invention related to methods of producing a C4-dicarboxylic acid (e.g., malic acid), comprising: (a) cultivating a recombinant host cell (e.g., a filamentous fungal host cell) having bicarbonate transporter activity in a medium under suitable conditions to produce the C4-dicarboxylic acid; and (b) recovering the C4-dicarboxylic acid. In some aspects, the recombinant host cell comprises a heterologous polynucleotide encoding a bicarbonate transporter (e.g., a sulfate-bicarbonate transporter). In another aspect, the invention related to methods of producing a C4-dicarboxylic acid (e.g., malic acid) comprising (a) transforming into a host cell (e.g., a filamentous fungal host cell) a heterologous polynucleotide encoding a bicarbonate transporter described herein; (b) cultivating the transformed organism in a medium under suitable conditions to produce the C4-dicarboxylic acid; and (c) recovering the C4-dicarboxylic acid. In some aspects of the methods, the recombinant host cell further comprises a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter, a heterologous polynucleotide encoding a malate dehydrogenase, and/or a heterologous polynucleotide encoding a pyruvate carboxylase.

BRIEF DESCRIPTION OF THE FIGURES

FIG. 1 shows a restriction map of pShTh60.

FIG. 2 shows a restriction map of pAmFs69.

FIGS. 3A and 3B show the genomic nucleotide construct sequence and the deduced amino acid sequence of an *Aspergillus oryzae* NRRL 3488 bicarbonate transporter gene (bt1) (SEQ ID NOs: 1 and 2, respectively).

FIGS. 4A and 4B show the genomic nucleotide construct sequence and the deduced amino acid sequence of an *Aspergillus oryzae* NRRL 3488 bicarbonate transporter gene (bt2) (SEQ ID NOs: 3 and 4, respectively).

FIG. 5 shows a restriction map of pSaMF36.

FIG. 6 shows the genomic DNA sequence and the deduced amino acid sequence of an *Aspergillus aculeatus* C4-dicarboxylic acid transporter gene (c4t521) (SEQ ID NOs: 5 and 6, respectively).

FIG. 7 shows the genomic DNA sequence and the deduced amino acid sequence of an *Aspergillus oryzae* NRRL 3488 malate dehydrogenase gene (mdh3) (SEQ ID NOs: 7 and 8, respectively).

FIG. 8 shows a restriction map of pSaMF21.

FIGS. 9A and 9B together show the genomic DNA sequence and the deduced amino acid sequence of an *Aspergillus oryzae* NRRL 3488 pyruvate carboxylase gene (pyc) (SEQ ID NOs: 9 and 10, respectively).

FIG. 10 shows a restriction map of pRYAN1.

FIG. 11 shows a restriction map of pShTh77.

FIG. 12 shows a restriction map of pShTh147.

DEFINITIONS

Bicarbonate transporter: The term “bicarbonate transporter” is defined herein as a protein—such as a membrane integrated protein—capable of facilitating the transfer of HCO_3^- across a biological membrane, such as a cell membrane and/or the membrane of a cell organelle. Non-limiting classes of bicarbonate transporter proteins include the anion exchanger (AE) family of $\text{Cl}^-/\text{HCO}_3^-$ exchangers, the NBC family of $\text{Na}^+/\text{HCO}_3^-$ cotransporters, and the Na^+ -dependent $\text{Cl}^-/\text{HCO}_3^-$ exchangers. In some aspects described herein, the bicarbonate transporter is a sulfate-

bicarbonate transporter, wherein the transporter is capable of facilitating the transfer of both HCO_3^- and SO_4^{2-} anions across a biological membrane. Biocarbonate exchange activity can be determined as described in the art, e.g., as described in Sterling et al., 2002, *Am J Physiol Cell Physiol* 283: C1522-1529.

The bicarbonate transporters have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% of the bicarbonate transporter activity of the mature polypeptide sequence of SEQ ID NO: 2 or 4.

C4-dicarboxylic acid transporter: The term “C4-dicarboxylic acid transporter” is defined herein as a dicarboxylic acid permease that can transport malic acid, succinic acid, oxaloacetic acid, malonic acid, and/or fumaric acid outside a cell (Grobler et al., 1995, *Yeast* 11: 1485-1491; Camarasa et al., 2001, *Applied and Environmental Microbiology* 67: 4144-4151). A computational method to predict mitochondrially imported proteins and their targeting sequences is described by Claros and Vincens, 1996, *Eur. J. Biochem.* 241: 779-786.

The C4-dicarboxylic acid transporters have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% of the C4-dicarboxylic acid transporter activity (e.g., malic acid transporter activity) of the mature polypeptide sequence of SEQ ID NO: 6.

Malate dehydrogenase: The term “malate dehydrogenase” is defined herein as a malate:NAD⁺ oxidoreductase (EC 1.1.1.37) that catalyzes the reduction of oxaloacetate in the presence of NADH+H⁺ to malate and NAD⁺. For purposes of the present invention, malate dehydrogenase activity is determined according to the following procedure. The assay solution consists of 1 mM oxaloacetic acid, 100 mM Tris pH 8.0, 10 mM NaHCO_3 , 5 mM MgCl_2 , and 0.1 mM NADH (Sigma Chemical Co., St. Louis, Mo., USA). The assay solution without oxaloacetic acid as substrate is run as a control to measure background NADH degradation rates. Dilutions of 1/100, 1/500, 1/2500, and 1/12500 of each supernatant are prepared with double-distilled water. Aliquots of 270 μl of the assay solution are dispensed into 96 well polystyrene flat bottom plates. A 30 μl sample of each diluted supernatant is added to initiate the assay. The reactions are monitored using a SPECTRAMAX® 340PC plate reader (Molecular Devices, Sunnyvale, Calif., USA) with the following settings: 340 nm, kinetic reading. A concentration series of NADH is used to construct a standard curve and a dilution series of purified malic dehydrogenase (Sigma Chemical Co., St. Louis, Mo., USA) is used as a positive control. One unit of malate dehydrogenase activity equals the amount of enzyme capable of converting 1 μmole of oxaloacetate and NADH+H⁺ to malate and NAD⁺ per minute at pH 8.0, 25° C.

The malate dehydrogenases have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% of the malate dehydrogenase activity of the mature polypeptide sequence of SEQ ID NO: 8.

Pyruvate carboxylase: The term “pyruvate carboxylase” is defined herein as a pyruvate:carbon-dioxide ligase (ADP-forming) (EC 6.4.1.1) that catalyzes the carboxylation of pyruvate in the presence of ATP and HCO_3^- to oxaloacetate,

ADP, and phosphate. For purposes of the present invention, pyruvate carboxylase activity is determined according to the procedure of the SIGMA® Quality Control Test procedure for pyruvate carboxylase (Sigma Chemical Co., St. Louis, Mo., USA) except the assay uses Tris buffer at pH 8.0. One unit of pyruvate carboxylase activity equals the amount of enzyme capable of converting 1 μ mole of pyruvate and CO₂ to oxaloacetate per minute at pH 7.8, 30° C.

The pyruvate carboxylases have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100% of the pyruvate carboxylase activity of the mature polypeptide sequence of SEQ ID NO: 10.

Heterologous polynucleotide: The term “heterologous polynucleotide” is defined herein as a polynucleotide that is not native to the host cell; a native polynucleotide in which structural modifications have been made to the coding region; a native polynucleotide whose expression is quantitatively altered as a result of a manipulation of the DNA by recombinant DNA techniques, e.g., a different (foreign) promoter; or a native polynucleotide whose expression is quantitatively altered by the introduction of one or more (several) extra copies of the polynucleotide into the host cell.

Isolated/purified: The terms “isolated” and “purified” mean a polypeptide or polynucleotide that is removed from at least one component with which it is naturally associated. For example, a polypeptide may be at least 1% pure, e.g., at least 5% pure, at least 10% pure, at least 20% pure, at least 40% pure, at least 60% pure, at least 80% pure, at least 90% pure, at least 93% pure, at least 95% pure, at least 97%, at least 98% pure, or at least 99% pure, as determined by SDS-PAGE and a polynucleotide may be at least 1% pure, e.g., at least 5% pure, at least 10% pure, at least 20% pure, at least 40% pure, at least 60% pure, at least 80% pure, at least 90%, at least 93% pure, at least 95% pure, at least 97%, at least 98% pure, or at least 99% pure, as determined by agarose electrophoresis.

Coding sequence: The term “coding sequence” means a polynucleotide sequence, which specifies the amino acid sequence of a polypeptide. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon or alternative start codons such as GTG and TTG and ends with a stop codon such as TAA, TAG, and TGA. The coding sequence may be a sequence of genomic DNA, cDNA, a synthetic polynucleotide, and/or a recombinant polynucleotide.

cDNA sequence: The term “cDNA sequence” means a sequence of DNA following reverse transcription from a mature, spliced, mRNA molecule obtained from a eukaryotic cell. The initial, primary RNA transcript from genomic DNA is a precursor to mRNA that is processed through a series of steps, including splicing, before appearing as mature spliced mRNA. A cDNA sequence lacks intervening intron sequences that may be present in the corresponding genomic DNA sequence. Accordingly, the phrase “the cDNA sequence of SEQ ID NO: X” intends the resulting sequence after the intervening intron sequences of SEQ ID NO: X, if present, are removed. In some instances—when a referenced genomic DNA sequence lacks intervening intron sequences—a cDNA sequence may be identical to its corresponding genomic DNA sequence.

Genomic DNA sequence. The term “genomic DNA sequence” means a DNA sequence found in the genome of a source organism (e.g., a eukaryotic or prokaryotic

genome). In some instances, a genomic DNA sequence from a eukaryotic genome contains one or more intervening intron sequences that are removed from the primary RNA transcript as a result of RNA splicing. Accordingly, the phrase “the genomic DNA sequence of SEQ ID NO: Y” intends the corresponding DNA sequence from the source organism which includes intervening intron sequences, if any, that are present before RNA splicing.

Mature polypeptide sequence: The term “mature polypeptide sequence” means the portion of the referenced polypeptide sequence after any post-translational sequence modifications (such as N-terminal processing and/or C-terminal truncation). In some instances, the mature polypeptide sequence may be identical to the entire referenced polypeptide sequence. In one aspect, the mature polypeptide sequence is amino acids 1 to 770 of SEQ ID NO: 2 based on the SignalP program (Nielsen et al., 1997, *Protein Engineering* 10: 1-6) and the InterProScan program (The European Bioinformatics Institute) that predicts the absence of a signal peptide. In another aspect, the mature polypeptide sequence is amino acids 1 to 843 of SEQ ID NO: 4 based on the SignalP program and the InterProScan program that predicts the absence of a signal peptide. It is known in the art that a host cell may produce a mixture of two or more different mature polypeptide sequences (i.e., with a different C-terminal and/or N-terminal amino acid) expressed by the same polynucleotide.

Mature polypeptide coding sequence: The term “mature polypeptide coding sequence” means the portion of the referenced polynucleotide sequence (e.g., genomic or cDNA sequence) that encodes a mature polypeptide sequence. In some instances, the mature polypeptide coding sequence may be identical to the entire referenced polynucleotide sequence. In one aspect, the mature polypeptide coding sequence is nucleotides 1 to 2503 of SEQ ID NO: 1 based on the SignalP program (supra) and the InterProScan program (supra) that predicts the absence of a signal peptide coding sequence. In another aspect, the mature polypeptide coding sequence is nucleotides 1 to 2657 of SEQ ID NO: 3 based on the SignalP program and the InterProScan program that predicts the absence of a signal peptide coding sequence.

Fragment: The term “fragment” means a polypeptide having one or more (several) amino acids deleted from the amino and/or carboxyl terminus of a referenced polypeptide sequence. In one aspect, the fragment has bicarbonate transporter activity. In another aspect, a fragment contains at least 650 amino acid residues, e.g., at least 690 amino acid residues or at least 730 amino acid residues of SEQ ID NO: 2. In another aspect, a fragment contains at least 720 amino acid residues, e.g., at least 760 amino acid residues or at least 800 amino acid residues of SEQ ID NO: 4.

Subsequence: The term “subsequence” means a polynucleotide having one or more (several) nucleotides deleted from the 5' and/or 3' end of the referenced nucleotide sequence. In one aspect, the subsequence encodes a fragment having bicarbonate transporter activity. In another aspect, a subsequence contains at least 1950 nucleotides, e.g., at least 2070 nucleotides or at least 2190 nucleotides of SEQ ID NO: 1. In another aspect, a subsequence contains at least 2160 nucleotides, e.g., at least 2280 nucleotides or at least 2400 nucleotides of SEQ ID NO: 3.

Allelic variant: The term “allelic variant” means any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the

encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

Sequence Identity: The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter "sequence identity".

For purposes of the present invention, the degree of sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *J. Mol. Biol.* 48: 443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *Trends Genet.* 16: 276-277), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labeled "longest identity" (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:

$$\frac{(\text{Identical Residues} \times 100)}{(\text{Length of Alignment} - \text{Total Number of Gaps in Alignment})}$$

For purposes of the present invention, the degree of sequence identity between two deoxyribonucleotide sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *supra*) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *supra*), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labeled "longest identity" (obtained using the -nobrief option) is used as the percent identity and is calculated as follows:

$$\frac{(\text{Identical Deoxyribonucleotides} \times 100)}{(\text{Length of Alignment} - \text{Total Number of Gaps in Alignment})}$$

Expression: The term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

Nucleic acid construct: The term "nucleic acid construct" means a nucleic acid molecule—single-stranded or double-stranded—which is isolated from a naturally occurring gene, modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature, or synthetic, wherein the nucleic acid molecule comprises one or more (several) control sequences.

Control sequence: The term "control sequence" means a nucleic acid sequence necessary for polypeptide expression. Control sequences may be native or foreign to the polynucleotide encoding the polypeptide, and native or foreign to each other. Such control sequences include, but are not limited to, a leader sequence, polyadenylation sequence, propeptide sequence, promoter sequence, signal peptide sequence, and transcription terminator sequence. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a polypeptide.

Operably linked: The term "operably linked" means a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of a

polynucleotide such that the control sequence directs the expression of the coding sequence.

Expression vector: The term "expression vector" means a linear or circular DNA molecule that comprises a polynucleotide encoding a polypeptide and is operably linked to control sequences, wherein the control sequences provide for expression of the polynucleotide encoding the polypeptide. At a minimum, the expression vector comprises a promoter sequence, and transcriptional and translational stop signal sequences.

Host cell: The term "host cell" means any cell type that is susceptible to transformation, transfection, transduction, and the like with a nucleic acid construct or expression vector comprising a polynucleotide of the present invention (e.g., a polynucleotide encoding a bicarbonate transporter). The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication.

Variant: The term "variant" means a polypeptide having activity, e.g., bicarbonate transporter activity, comprising an alteration, i.e., a substitution, insertion, and/or deletion of one or more (several) amino acid residues at one or more (several) positions. A substitution means a replacement of an amino acid occupying a position with a different amino acid; a deletion means removal of an amino acid occupying a position; and an insertion means adding one or more (several), e.g., 1-3 amino acids, adjacent to an amino acid occupying a position.

Volumetric productivity: The term "volumetric productivity" refers to the amount of referenced product produced (e.g., the amount of a C4-dicarboxylic acid produced) per volume of the system used (e.g., the total volume of media and contents therein) per unit of time.

Fermentable medium: The term "fermentable medium" refers to a medium comprising one or more (several) sugars, such as glucose, fructose, sucrose, cellobiose, xylose, xylulose, arabinose, mannose, galactose, and/or soluble oligosaccharides, wherein the medium is capable, in part, of being converted (fermented) by a host cell into a desired product, such as a C4-dicarboxylic acid. In some instances, the fermentation medium is derived from a natural source, such as sugar cane, starch, or cellulose, and may be the result of pretreating the source by enzymatic hydrolysis (saccharification).

Reference to "about" a value or parameter herein includes aspects that are directed to that value or parameter per se. For example, description referring to "about X" includes the aspect "X".

As used herein and in the appended claims, the singular forms "a," "or," and "the" include plural referents unless the context clearly dictates otherwise. It is understood that the aspects of the invention described herein include "consisting" and/or "consisting essentially of" aspects.

Unless defined otherwise or clearly indicated by context, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

DETAILED DESCRIPTION OF THE INVENTION

The present invention describes, inter alia, the overexpression of specific genes in a host cell, such as a filamentous fungus (e.g., *Aspergillus*) to enhance the production of C4-dicarboxylic acids (e.g., malic acid). The invention encompasses the use of a heterologous gene for the expression of a bicarbonate transporter. The bicarbonate trans-

porter can be any described bicarbonate transporter that is suitable for practicing the present invention. In one aspect, the bicarbonate transporter is a transporter that is overexpressed under culture conditions that produces C4-dicarboxylic acid in high titers. In one aspect, the bicarbonate transporter is a sulfate-bicarbonate transporter. The recombinant host cell may further comprise a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter; a heterologous polynucleotide encoding a malate dehydrogenase; and/or a heterologous polynucleotide encoding a pyruvate carboxylase.

Bicarbonate Transporters and Polynucleotides Encoding Bicarbonate Transporters

In one aspect of the recombinant host cells and methods described herein, the bicarbonate transporter is selected from the group consisting of: (a) a bicarbonate transporter having at least 60% sequence identity to SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof; (b) a bicarbonate transporter encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii); (c) a bicarbonate transporter encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v); (d) a bicarbonate transporter variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has bicarbonate transporter activity.

In one aspect, the bicarbonate transporter comprises or consists of an amino acid sequence of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof. In one aspect, the bicarbonate transporter comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof.

In one aspect, the bicarbonate transporter comprises or consists of an amino acid sequence of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2 or the mature polypeptide sequence thereof. In one aspect, the bicarbonate transporter comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 2 or the mature polypeptide sequence thereof. In another aspect, the bicarbonate transporter comprises an amino acid sequence of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 4 or the

mature polypeptide sequence thereof. In one aspect, the bicarbonate transporter comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 4 or the mature polypeptide sequence thereof.

In one aspect, the bicarbonate transporter comprises or consists of the amino acid sequence of SEQ ID NO: 2, the mature polypeptide sequence of SEQ ID NO: 2, an allelic variant thereof, or a fragment of the foregoing, having bicarbonate transporter activity. In another aspect, the bicarbonate transporter comprises or consists of the amino acid sequence of SEQ ID NO: 2. In another aspect, the bicarbonate transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 2. In another aspect, the bicarbonate transporter comprises or consists of amino acids 1 to 770 of SEQ ID NO: 2.

In one aspect, the bicarbonate transporter comprises or consists of the amino acid sequence of SEQ ID NO: 4, the mature polypeptide sequence of SEQ ID NO: 4, an allelic variant thereof, or a fragment of the foregoing, having bicarbonate transporter activity. In another aspect, the bicarbonate transporter comprises or consists of the amino acid sequence of SEQ ID NO: 4. In another aspect, the bicarbonate transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 4. In another aspect, the bicarbonate transporter comprises or consists of amino acids 1 to 843 of SEQ ID NO: 4.

In one aspect, the bicarbonate transporter is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii) (see, e.g., J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, N.Y.).

In one aspect, the bicarbonate transporter is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 1 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii). In another aspect, the bicarbonate transporter is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 3 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 3 or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii).

In one aspect, the bicarbonate transporter is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

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In one aspect, the bicarbonate transporter is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 1 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

In one aspect, the bicarbonate transporter is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 3 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 3 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

In one aspect, the bicarbonate transporter is encoded by SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof. In one aspect, the bicarbonate transporter is encoded by SEQ ID NO: 1 or the mature polypeptide coding sequence thereof. In one aspect, the bicarbonate transporter is encoded by SEQ ID NO: 1. In one aspect, the bicarbonate transporter is encoded by SEQ ID NO: 3 or the mature polypeptide coding sequence thereof. In one aspect, the bicarbonate transporter is encoded by SEQ ID NO: 3. In one aspect, the bicarbonate transporter is encoded by a subsequence of SEQ ID NO: 1 or 3, wherein the subsequence encodes a polypeptide having bicarbonate transporter activity. In one aspect, the bicarbonate transporter is encoded by a subsequence of SEQ ID NO: 1, wherein the subsequence encodes a polypeptide having bicarbonate transporter activity. In one aspect, the bicarbonate transporter is encoded by a subsequence of SEQ ID NO: 3, wherein the subsequence encodes a polypeptide having bicarbonate transporter activity.

In one aspect, the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof. In one aspect, the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2. In one aspect, the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 2. In one aspect, the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 4. In one aspect, the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 4.

Preferably, amino acid changes are of a minor nature, that is conservative amino acid substitutions or insertions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of one to about 30 amino acids; small amino-terminal or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to about 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

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Examples of conservative substitutions are within the group of basic amino acids (arginine, lysine and histidine), acidic amino acids (glutamic acid and aspartic acid), polar amino acids (glutamine and asparagine), hydrophobic amino acids (leucine, isoleucine and valine), aromatic amino acids (phenylalanine, tryptophan and tyrosine), and small amino acids (glycine, alanine, serine, threonine and methionine). Amino acid substitutions that do not generally alter specific activity are known in the art and are described, for example, by H. Neurath and R. L. Hill, 1979, *In, The Proteins*, Academic Press, New York. The most commonly occurring exchanges are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly.

Alternatively, the amino acid changes are of such a nature that the physico-chemical properties of the polypeptides are altered. For example, amino acid changes may improve the thermal stability of the polypeptide, alter the substrate specificity, change the pH optimum, and the like.

Essential amino acids in a parent polypeptide can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, 1989, *Science* 244: 1081-1085). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant molecules are tested for bicarbonate transporter activity to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton et al., 1996, *J. Biol. Chem.* 271: 4699-4708. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction, or photoaffinity labeling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos et al., 1992, *Science* 255: 306-312; Smith et al., 1992, *J. Mol. Biol.* 224: 899-904; Wlodaver et al., 1992, *FEBS Lett.* 309: 59-64. The identities of essential amino acids can also be inferred from analysis of identities with polypeptides that are related to the referenced parent polypeptide.

Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86: 2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (e.g., Lowman et al., 1991, *Biochemistry* 30: 10832-10837; U.S. Pat. No. 5,223,409; WO 92/06204), and region-directed mutagenesis (Derbyshire et al., 1986, *Gene* 46: 145; Ner et al., 1988, *DNA* 7: 127).

Mutagenesis/shuffling methods can be combined with high-throughput, automated screening methods to detect activity of cloned, mutagenized polypeptides expressed by host cells (Ness et al., 1999, *Nature Biotechnology* 17: 893-896). Mutagenized DNA molecules that encode active polypeptides can be recovered from the host cells and rapidly sequenced using standard methods in the art. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide.

In some aspects, the total number of amino acid substitutions, deletions and/or insertions of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof, is not more than 10, e.g., not more than 1, 2, 3, 4, 5, 6, 7, 8 or 9.

In another aspect, the bicarbonate transporter is a fragment of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof, wherein the fragment has bicarbonate

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transporter activity. In one aspect, the bicarbonate transporter is a fragment of SEQ ID NO: 2 or the mature polypeptide sequence thereof, wherein the fragment has bicarbonate transporter activity. In one aspect, the fragment contains at least 650 amino acid residues, e.g., preferably at least 690 amino acid residues, or at least 730 amino acid residues of SEQ ID NO: 2. In one aspect, the fragment contains a bicarbonate transporter domain, e.g., the putative transporter domain of amino acids 280 to 556 of SEQ ID NO: 2. In another aspect, the bicarbonate transporter is a fragment of SEQ ID NO: 4 or the mature polypeptide sequence thereof, wherein the fragment has bicarbonate transporter activity. In one aspect, the fragment contains at least 720 amino acid residues, e.g., preferably at least 760 amino acid residues, or at least 800 amino acid residues of SEQ ID NO: 4. In one aspect, the fragment contains a bicarbonate transporter domain, e.g., the putative transporter domain of amino acids 192 to 480 of SEQ ID NO: 4.

The bicarbonate transporter may be a fused polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of the present invention. A fused polypeptide is produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fused polypeptide is under control of the same promoter(s) and terminator. Fusion proteins may also be constructed using intein technology in which fusions are created post-translationally (Cooper et al., 1993, *EMBO J.* 12: 2575-2583; Dawson et al., 1994, *Science* 266: 776-779).

A fusion polypeptide can further comprise a cleavage site between the two polypeptides. Upon secretion of the fusion protein, the site is cleaved releasing the two polypeptides. Examples of cleavage sites include, but are not limited to, the sites disclosed in Martin et al., 2003, *J. Ind. Microbiol. Biotechnol.* 3: 568-576; Svetina et al., 2000, *J. Biotechnol.* 76: 245-251; Rasmussen-Wilson et al., 1997, *Appl. Environ. Microbiol.* 63: 3488-3493; Ward et al., 1995, *Biotechnology* 13: 498-503; and Contreras et al., 1991, *Biotechnology* 9: 378-381; Eaton et al., 1986, *Biochemistry* 25: 505-512; Collins-Racie et al., 1995, *Biotechnology* 13: 982-987; Carter et al., 1989, *Proteins: Structure, Function, and Genetics* 6: 240-248; and Stevens, 2003, *Drug Discovery World* 4: 35-48.

Techniques used to isolate or clone a polynucleotide—such as a polynucleotide encoding a bicarbonate transporter—as well as any other polypeptide used in any of the aspects mentioned herein, are known in the art and include isolation from genomic DNA, preparation from cDNA, or a combination thereof. The cloning of the polynucleotides from such genomic DNA can be effected, e.g., by using the well known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shares structural features. See, e.g., Innis et al., 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligated activated transcription (LAT) and nucleotide sequence-based amplification (NASBA) may be used. The polynucleotides may be cloned from a strain of *Aspergillus*, or another or related organism, and thus, for example, may be an allelic or species variant of the polypeptide encoding region of the nucleotide sequence.

The polynucleotide of SEQ ID NO: 1 or 3, or a subsequence thereof; as well as the amino acid sequence of SEQ

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ID NO: 2 or 4; or a fragment thereof; may be used to design nucleic acid probes to identify and clone DNA encoding a bicarbonate transporter from strains of different genera or species according to methods well known in the art. In particular, such probes can be used for hybridization with the genomic or cDNA of the genus or species of interest, following standard Southern blotting procedures, in order to identify and isolate the corresponding gene therein. Such probes can be considerably shorter than the entire sequence, e.g., at least 14 nucleotides, at least 25 nucleotides, at least 35 nucleotides, at least 70 nucleotides in lengths. The probes may be longer, e.g., at least 100 nucleotides, at least 200 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides in lengths. Even longer probes may be used, e.g., at least 600 nucleotides, at least 700 nucleotides, at least 800 nucleotides, or at least 900 nucleotides in length. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene (for example, with ^{32}P , ^3H , ^{35}S , biotin, or avidin). Such probes are encompassed by the present invention.

A genomic DNA or cDNA library prepared from such other strains may be screened for DNA that hybridizes with the probes described above and encodes a polypeptide having bicarbonate transporter activity. Genomic or other DNA from such other strains may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be transferred to and immobilized on nitrocellulose or other suitable carrier material. In order to identify a clone or DNA that is homologous with SEQ ID NO: 1 or 3, or a subsequence thereof, the carrier material is preferably used in a Southern blot.

For purposes of the present invention, hybridization indicates that the polynucleotide hybridizes to a labeled nucleic acid probe corresponding to SEQ ID NO: 1 or 3, the mature polypeptide coding sequence of SEQ ID NO: 1 or 3, or the full-length complementary strand thereof, or a subsequence of the foregoing; under very low to very high stringency conditions. Molecules to which the nucleic acid probe hybridizes under these conditions can be detected using, for example, X-ray film.

In one aspect, the nucleic acid probe is SEQ ID NO: 1 or 3. In another aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 1 or 3. In another aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 1. In another aspect, the nucleic acid probe is SEQ ID NO: 1. In another aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 3. In another aspect, the nucleic acid probe is SEQ ID NO: 3. In another aspect, the nucleic acid probe is a polynucleotide that encodes the polypeptide of SEQ ID NO: 2 or a fragment thereof. In another aspect, the nucleic acid probe is a polynucleotide that encodes the polypeptide of SEQ ID NO: 4 or a fragment thereof.

For long probes of at least 100 nucleotides in length, very low to very high stringency conditions are defined as pre-hybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/mL sheared and denatured salmon sperm DNA, and either 25% formamide for very low and low stringencies, 35% formamide for medium and medium-high stringencies, or 50% formamide for high and very high stringencies, following standard Southern blotting procedures for 12 to 24 hours optimally. The carrier material is finally washed three times each for 15 minutes using 2×SSC, 0.2% SDS at 45° C. (very low stringency), at 50° C. (low stringency), at 55° C. (medium stringency), at 60° C. (me-

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dium-high stringency), at 65° C. (high stringency), and at 70° C. (very high stringency).

For short probes of about 15 nucleotides to about 70 nucleotides in length, stringency conditions are defined as prehybridization and hybridization at about 5° C. to about 10° C. below the calculated T_m using the calculation according to Bolton and McCarthy (1962, *Proc. Natl. Acad. Sci. USA* 48:1390) in 0.9 M NaCl, 0.09 M Tris-HCl pH 7.6, 6 mM EDTA, 0.5% NP-40, 1×Denhardt's solution, 1 mM sodium pyrophosphate, 1 mM sodium monobasic phosphate, 0.1 mM ATP, and 0.2 mg of yeast RNA per mL following standard Southern blotting procedures for 12 to 24 hours optimally. The carrier material is finally washed once in 6×SSC plus 0.1% SDS for 15 minutes and twice each for 15 minutes using 6×SSC at 5° C. to 10° C. below the calculated T_m .

The bicarbonate transporter of the present invention may be obtained from a microorganism of any genus. As used herein, the term "obtained from" in connection with a given source shall mean that the polypeptide encoded by a polynucleotide is produced by the source or by a cell in which the polynucleotide from the source has been inserted.

The bicarbonate transporter may be a bacterial bicarbonate transporter. For example, the bicarbonate transporter may be a Gram-positive bacterial polypeptide such as a *Bacillus*, *Streptococcus*, *Streptomyces*, *Staphylococcus*, *Enterococcus*, *Lactobacillus*, *Lactococcus*, *Clostridium*, *Geobacillus*, or *Oceanobacillus* bicarbonate transporter, or a Gram-negative bacterial polypeptide such as an *E. coli*, *Pseudomonas*, *Salmonella*, *Campylobacter*, *Helicobacter*, *Flavobacterium*, *Fusobacterium*, *Ilyobacter*, *Neisseria*, or *Ureaplasma* bicarbonate transporter.

In one aspect, the bicarbonate transporter is a *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis* bicarbonate transporter.

In another aspect, the bicarbonate transporter is a *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, or *Streptococcus equi* subsp. *Zooepidemicus* bicarbonate transporter. In another aspect, the bicarbonate transporter is a *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, or *Streptomyces lividans* bicarbonate transporter.

The bicarbonate transporter may be a fungal bicarbonate transporter. In one aspect, the fungal bicarbonate transporter is a yeast bicarbonate transporter such as a *Candida*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* bicarbonate transporter.

In another aspect, the fungal bicarbonate transporter is a filamentous fungal bicarbonate transporter such as an *Acremonium*, *Agaricus*, *Alternaria*, *Aspergillus*, *Aureobasidium*, *Botryosphaeria*, *Ceriporiopsis*, *Chaetomidium*, *Chrysosporium*, *Claviceps*, *Cochliobolus*, *Coprinopsis*, *Coptotermes*, *Corynascus*, *Cryphonectria*, *Cryptococcus*, *Diplodia*, *Exidia*, *Filibasidium*, *Fusarium*, *Gibberella*, *Holomastigotoides*, *Humicola*, *Irpex*, *Lentinula*, *Leptosphaeria*, *Magnaporthe*, *Melanocarpus*, *Meripilus*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Piromyces*, *Poitrasia*, *Pseudoplectanina*, *Pseudotrichonympha*, *Rhizomucor*, *Schizophyllum*, *Scytalidium*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trichoderma*, *Trichophaea*, *Verticillium*, *Volvariella*, or *Xylaria* bicarbonate transporter.

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In another aspect, the bicarbonate transporter is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, or *Saccharomyces oviformis* bicarbonate transporter.

In another aspect, the bicarbonate transporter is an *Acremonium cellulolyticus*, *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus flavus*, *Aspergillus fumigatus*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Aspergillus sojae*, *Chrysosporium keratinophilum*, *Chrysosporium lucknowense*, *Chrysosporium tropicum*, *Chrysosporium merdarium*, *Chrysosporium inops*, *Chrysosporium pannicola*, *Chrysosporium queenslandicum*, *Chrysosporium zonatum*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola grisea*, *Humicola insolens*, *Humicola lanuginosa*, *Irpex lacteus*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium funiculosum*, *Penicillium purpurogenum*, *Phanerochaete chrysosporium*, *Thielavia achromatica*, *Thielavia albomyces*, *Thielavia albopilosa*, *Thielavia australeinsis*, *Thielavia fimeti*, *Thielavia microspora*, *Thielavia ovispora*, *Thielavia peruviana*, *Thielavia speditonum*, *Thielavia setosa*, *Thielavia subthermophila*, *Thielavia terrestris*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* bicarbonate transporter.

In one aspect, the bicarbonate transporter is an *Aspergillus* bicarbonate transporter, such as an *Aspergillus oryzae* bicarbonate transporter. In one aspect, the bicarbonate transporter is an *Aspergillus oryzae* bicarbonate transporter of SEQ ID NO: 2. In another aspect, the bicarbonate transporter is an *Aspergillus oryzae* bicarbonate transporter of SEQ ID NO: 4.

It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states, and other taxonomic equivalents, e.g., anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents.

Strains of these species are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

The bicarbonate transporter may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms and DNA directly from natural habitats are well known in the art. The polynucleotide encoding a bicarbonate transporter may then be derived by similarly screening a genomic or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a bicarbonate transporter has been detected with suitable probe(s) as described herein, the sequence may be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, e.g.,

J. Sambrook, E. F. Fritsch, and T. Maniatus, 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, N.Y.).

C4-Dicarboxylic Acid Transporters and Polynucleotides Encoding C4-Dicarboxylic Acid Transporters

In some aspects of the recombinant host cells and methods of use thereof, the host cells have C4-dicarboxylic acid transporter activity. In some aspects, the host cells comprise a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter. The C4-dicarboxylic acid transporter can be any C4-dicarboxylic acid transporter that is suitable for practicing the invention. In one aspect, the C4-dicarboxylic acid transporter is present in the cytosol of the host cell.

In one aspect, the C4-dicarboxylic acid transporter is (a) a C4-dicarboxylic acid transporter having at least 60% sequence identity to SEQ ID NO: 6 or the mature polypeptide sequence thereof; (b) a C4-dicarboxylic acid transporter encoded by a polynucleotide that hybridizes under low stringency conditions with SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing; (c) a C4-dicarboxylic acid transporter encoded by a polynucleotide having at least 60% sequence identity to SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing; (d) a C4-dicarboxylic acid transporter variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 6 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has C4-dicarboxylic acid transporter activity.

In one aspect, the C4-dicarboxylic acid transporter comprises or consists of an amino acid sequence having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 6 or the mature polypeptide sequence thereof. In one aspect, the C4-dicarboxylic acid transporter comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 6 or the mature polypeptide sequence thereof.

In one aspect, the C4-dicarboxylic acid transporter comprises or consists of the amino acid sequence of SEQ ID NO: 6, the mature polypeptide sequence of SEQ ID NO: 6, an allelic variant thereof, or a fragment of the foregoing, having C4-dicarboxylic acid transporter activity. In another aspect, the C4-dicarboxylic acid transporter comprises or consists of the amino acid sequence of SEQ ID NO: 6. In another aspect, the C4-dicarboxylic acid transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 6. In another aspect, the C4-dicarboxylic acid transporter comprises or consists of amino acids 1 to 418 of SEQ ID NO: 6. In another aspect, the C4-dicarboxylic acid transporter comprises or consists of amino acids 18 to 418 of SEQ ID NO: 6.

In one aspect, the C4-dicarboxylic acid transporter is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing (J. Sambrook, E.F. Fritsch, and T. Maniatis, 1989, supra).

In one aspect, the C4-dicarboxylic acid transporter is encoded by a polynucleotide having at least 65%, e.g., at

least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing.

In one aspect, the C4-dicarboxylic acid transporter is encoded by SEQ ID NO: 5 or the mature polypeptide coding sequence thereof. In one aspect, the C4-dicarboxylic acid transporter is encoded by SEQ ID NO: 5. In one aspect, the C4-dicarboxylic acid transporter is encoded by the mature polypeptide coding sequence of SEQ ID NO: 5. In one aspect, the mature polypeptide coding sequence is nucleotides 1 to 1257 of SEQ ID NO: 5. In one aspect, the mature polypeptide coding sequence is nucleotides 52 to 1257 of SEQ ID NO: 5. In one aspect, the C4-dicarboxylic acid transporter is encoded by a subsequence of SEQ ID NO: 5, wherein the subsequence encodes a polypeptide having C4-dicarboxylic acid transporter activity. In one aspect, the subsequence contains at least 1065 nucleotides, e.g., at least 1125 nucleotides or at least 1185 nucleotides of SEQ ID NO: 5.

In one aspect, the C4-dicarboxylic acid transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 6 or the mature polypeptide sequence thereof, as described supra. In one aspect, the C4-dicarboxylic acid transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 6. In one aspect, the C4-dicarboxylic acid transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 6. In some aspects, the total number of amino acid substitutions, deletions and/or insertions of SEQ ID NO: 6 or the mature polypeptide sequence thereof is not more than 10, e.g., not more than 1, 2, 3, 4, 5, 6, 7, 8 or 9.

In another aspect, the C4-dicarboxylic acid transporter is a fragment of SEQ ID NO: 6 or the mature polypeptide sequence thereof, wherein the fragment has C4-dicarboxylic acid transporter activity. In one aspect, the fragment contains at least 355 amino acid residues, e.g., at least 375 amino acid residues, or at least 395 amino acid residues of SEQ ID NO: 6.

The C4-dicarboxylic acid transporter may also be an allelic variant or artificial variant of a C4-dicarboxylic acid transporter.

The C4-dicarboxylic acid transporter can also include fused polypeptides or cleavable fusion polypeptides, as described supra.

Techniques used to isolate or clone a polynucleotide encoding a C4-dicarboxylic acid transporter are described supra.

The polynucleotide sequence of SEQ ID NO: 5 or a subsequence thereof; as well as the amino acid sequence of SEQ ID NO: 6 or a fragment thereof; may be used to design nucleic acid probes to identify and clone DNA encoding C4-dicarboxylic acid transporter from strains of different genera or species, as described supra. Such probes are encompassed by the present invention. A genomic DNA or cDNA library prepared from such other organisms may be screened for DNA that hybridizes with the probes described above and encodes a C4-dicarboxylic acid transporter, as described supra.

In one aspect, the nucleic acid probe is SEQ ID NO: 5. In another aspect, the nucleic acid probe is the mature polypeptide sequence of SEQ ID NO: 5. In another aspect, the

nucleic acid probe is a polynucleotide sequence that encodes SEQ ID NO: 6, the mature polypeptide sequence thereof, or a fragment of the foregoing.

For long probes of at least 100 nucleotides in length, very low to very high stringency and washing conditions are defined as described supra. For short probes of about 15 nucleotides to about 70 nucleotides in length, stringency and washing conditions are defined as described supra.

The C4-dicarboxylic acid transporter may be obtained from microorganisms of any genus. In one aspect, the C4-dicarboxylic acid transporter may be a bacterial, a yeast, or a filamentous fungal C4-dicarboxylic acid transporter obtained from the microorganisms described herein. In another aspect, the C4-dicarboxylic acid transporter is an *Aspergillus* C4-dicarboxylic acid transporter, such as an *Aspergillus aculeatus* C4-dicarboxylic acid transporter, e.g., the *Aspergillus aculeatus* C4-dicarboxylic acid transporter of SEQ ID NO: 6.

Other C4-dicarboxylic acid transporter that can be used with the host cells and methods of use described herein include, but are not limited to, the *Aspergillus flavus* C4 dicarboxylic acid transporter (AFLA_107340), the *Aspergillus oryzae* C4-dicarboxylic acid transporter of SEQ ID NO: 27 (encoded by the polynucleotide sequence of SEQ ID NO: 26; see US 2011/0053233), the *Aspergillus terreus* C4-dicarboxylic acid transporter of SEQ ID NO: 29 (encoded by the polynucleotide sequence of SEQ ID NO: 28; see US 2011/0053233), the *Schizosaccharomyces pombe* C4-dicarboxylic acid transporter of SEQ ID NO: 32 (encoded by the polynucleotide sequence of SEQ ID NO: 30 or 31; see US 2011/0053233), the *Aspergillus aculeatus* C4-dicarboxylic acid transporter of SEQ ID NO: 34 (encoded by the polynucleotide sequence of SEQ ID NO: 33; see U.S. application Ser. No. 13/165,696, entitled "Polypeptides Having C4-dicarboxylic acid Transporter Activity and Polynucleotides Encoding Same" filed Jun. 21, 2011), the *Aspergillus aculeatus* C4-dicarboxylic acid transporter of SEQ ID NO: 36 (encoded by the polynucleotide sequence of SEQ ID NO: 35; see U.S. application Ser. No. 13/165,696, supra), the *Schizosaccharomyces japonicus* C4-dicarboxylic acid transporter of SEQ ID NO: 39 (encoded by the polynucleotide sequence of SEQ ID NO: 37 or 38; see PCT/US11/38881, entitled "C4-dicarboxylic acid Production in Filamentous Fungi" filed Jun. 2, 2011), the *Aspergillus clavatus* C4-dicarboxylic acid transporter of SEQ ID NO: 41 (encoded by the polynucleotide sequence of SEQ ID NO: 40; see U.S. application Ser. No. 13/165,719, entitled "Methods for Improving C4-dicarboxylic acid Production in Filamentous Fungi" filed Jun. 21, 2011), the *Aspergillus fumigatus* C4-dicarboxylic acid transporter of SEQ ID NO: 43 (encoded by the polynucleotide sequence of SEQ ID NO: 42; see U.S. application Ser. No. 13/165,719, supra), or any aspect of the C4-dicarboxylic acid transporter described in the respective reference therein. Any aspect described herein related to sequence identity, hybridization, amino acid modifications (e.g., substitutions, deletions, and/or insertions), fragments or subsequences thereof is embraced for the C4-dicarboxylic acid transporters above.

The invention embraces any aspect of sequence identity, hybridization, variants and fragments described herein as applied to the C4-dicarboxylic acid transporter polypeptide sequences and polynucleotide sequences described above. For example, in one aspect, the C4-dicarboxylic acid transporter is (a) a C4-dicarboxylic acid transporter having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%,

at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 27, 29, 32, 34, 36, 39, 41, or 43, or the mature polypeptide sequence thereof; (b) a C4-dicarboxylic acid transporter encoded by a polynucleotide that hybridizes under low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 26, 28, 30, 31, 33, 35, 37, 38, 40, or 42, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 26, 28, 30, 31, 33, 35, 37, 38, 40, or 42, or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of the (i) or (ii); (c) a C4-dicarboxylic acid transporter encoded by a polynucleotide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 26, 28, 30, 31, 33, 35, 37, 38, 40, or 42, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 26, 28, 30, 31, 33, 35, 37, 38, 40, or 42, or the mature polypeptide coding sequence thereof, or (vi) the full-length complementary strand of the (iv) or (v); (d) a C4-dicarboxylic acid transporter variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 27, 29, 32, 34, 36, 39, 41, or 43, or the mature polypeptide sequence thereof; or (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has C4-dicarboxylic acid transporter activity.

The C4-dicarboxylic acid transporter may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) as described supra. Malate Dehydrogenases and Polynucleotides Encoding Malate Dehydrogenases

In some aspects of the recombinant host cells and methods of use thereof, the host cells have malate dehydrogenase activity. In some aspects, the host cells comprise a heterologous polynucleotide encoding a malate dehydrogenase. The malate dehydrogenase can be any malate dehydrogenase that is suitable for practicing the invention. In one aspect, the malate dehydrogenase is an enzyme that is present in the cytosol of the host cell.

In one aspect of the recombinant host cells and methods described herein, the malate dehydrogenase is (a) a malate dehydrogenase having at least 60% sequence identity to SEQ ID NO: 8 or the mature polypeptide sequence thereof; (b) a malate dehydrogenase encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii); (c) a malate dehydrogenase encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, or (vi) the full-length complementary strand of (iv) or (v); (d) a malate dehydrogenase variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 8 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has malate dehydrogenase activity.

In one aspect, the malate dehydrogenase comprises or consists of an amino acid sequence having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 8 or the mature polypeptide sequence thereof. In one aspect, the malate dehydrogenase comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 8 or the mature polypeptide sequence thereof.

In one aspect, the malate dehydrogenase comprises or consists of the amino acid sequence of SEQ ID NO: 8, the mature polypeptide sequence of SEQ ID NO: 8, an allelic variant thereof, or a fragment of the foregoing, having malate dehydrogenase activity. In another aspect, the malate dehydrogenase comprises or consists of the amino acid sequence of SEQ ID NO: 8. In another aspect, the malate dehydrogenase comprises or consists of the mature polypeptide sequence of SEQ ID NO: 8. In another aspect, the malate dehydrogenase comprises or consists of amino acids 1 to 330 of SEQ ID NO: 8.

In one aspect, the malate dehydrogenase is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii) (J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *supra*).

In one aspect, the malate dehydrogenase is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

In one aspect, the malate dehydrogenase is encoded by SEQ ID NO: 7, or the mature polypeptide coding sequence thereof. In one aspect, the malate dehydrogenase is encoded by SEQ ID NO: 7. In one aspect, the malate dehydrogenase is encoded by the mature polypeptide coding sequence of SEQ ID NO: 7. In one aspect, the malate dehydrogenase is encoded by a subsequence of SEQ ID NO: 7, wherein the subsequence encodes a polypeptide having malate dehydrogenase activity. In one aspect, the subsequence contains at least 885 nucleotides, e.g., at least 930 nucleotides or at least 975 nucleotides of SEQ ID NO: 7.

In one aspect, the malate dehydrogenase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 8, or the mature polypeptide sequence thereof, as described *supra*. In one aspect, the malate dehydrogenase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 8. In one aspect, the malate dehydrogenase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 8. In some aspects, the total number of amino acid substitutions, deletions and/or insertions of the mature polypeptide

sequence of SEQ ID NO: 8 or the mature polypeptide sequence thereof is not more than 10, e.g., not more than 1, 2, 3, 4, 5, 6, 7, 8 or 9.

In another aspect, the malate dehydrogenase is a fragment of SEQ ID NO: 8, or the mature polypeptide sequence thereof, wherein the fragment has malate dehydrogenase activity. In one aspect, the fragment contains at least 295 amino acid residues, e.g., at least 310 amino acid residues, or at least 325 amino acid residues of SEQ ID NO: 8.

The malate dehydrogenase may also be an allelic variant or artificial variant of a malate dehydrogenase.

The malate dehydrogenase can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Techniques used to isolate or clone a polynucleotide encoding a malate dehydrogenase are described *supra*.

The polynucleotide of SEQ ID NO: 7; or a subsequence thereof; as well as the amino acid sequence of SEQ ID NO: 8; or a fragment thereof; may be used to design nucleic acid probes to identify and clone DNA encoding malate dehydrogenases from strains of different genera or species, as described *supra*. Such probes are encompassed by the present invention. A genomic DNA or cDNA library prepared from such other organisms may be screened for DNA that hybridizes with the probes described above and encodes an malate dehydrogenase, as described *supra*.

In one aspect, the nucleic acid probe is SEQ ID NO: 7. In another aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 7. In another aspect, the nucleic acid probe is a polynucleotide sequence that encodes SEQ ID NO: 8, the mature polypeptide sequence thereof, or a fragment of the foregoing.

For long probes of at least 100 nucleotides in length, very low to very high stringency and washing conditions are defined as described *supra*. For short probes of about 15 nucleotides to about 70 nucleotides in length, stringency and washing conditions are defined as described *supra*.

The malate dehydrogenase may be obtained from microorganisms of any genus. In one aspect, the malate dehydrogenase may be a bacterial, a yeast, or a filamentous fungal malate dehydrogenase obtained from the microorganisms described herein. In another aspect, the malate dehydrogenase is an *Aspergillus oryzae* malate dehydrogenase, e.g., the *Aspergillus oryzae* malate dehydrogenase of SEQ ID NO: 8.

Other malate dehydrogenases that can be used to practice the present invention include, but are not limited to, a *Aspergillus nidulans* malate dehydrogenase (AN6717.1; SIMS et al., 2004, *Mycol. Res.* 108: 853-857); *Aspergillus niger* malate dehydrogenase (An16g00120; Pel et al., 2007, *Nature Biotechnology* 25: 221-231); *Phytophthora infestans* malate dehydrogenase (PITG 13614.1; Calcagno et al., 2009, *Mycological Research* 113: 771-781); *Saccharomyces cerevisiae* malate dehydrogenase (YKL085W; McAlister-Henn and Thompson, 1987, *J. Bacteriol.* 169: 5157-5166); *Talaromyces emersonii* malate dehydrogenase (AF439996, AF487682; Maloney et al., 2004, *Eur. J. Biochem.* 271: 3115-3126); and *Ustilago maydis* malate dehydrogenase (um00403, um11161; McCann and Snetselaar, 2008, *Fungal Genetics and Biology* 45: S77-S87), the *Aspergillus oryzae* malate dehydrogenase of SEQ ID NO: 45 (encoded by the polynucleotide sequence of SEQ ID NO: 44; see U.S. application Ser. No. 12/870,523, entitled "Methods for Improving Malic Acid Production in Filamentous Fungi" filed Aug. 27, 2010), or any aspect of the malate dehydrogenase described in the respective reference therein. Any aspect described herein related to sequence identity, hybridization, amino acid modifications (e.g., substitutions, dele-

tions, and/or insertions), fragments or subsequences thereof is embraced for the malate dehydrogenases above.

The invention embraces any aspect of sequence identity, hybridization, variants and fragments described herein as applied to the malate dehydrogenase polypeptide sequences and polynucleotide sequences described above. For example, in one aspect, the malate dehydrogenase is (a) a malate dehydrogenase having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 45, or the mature polypeptide sequence thereof; (b) a malate dehydrogenase encoded by a polynucleotide that hybridizes under low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 44 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 44 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of the (i) or (ii); (c) a malate dehydrogenase encoded by a polynucleotide having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 44 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 44 or the mature polypeptide coding sequence thereof, or (vi) the full-length complementary strand of the (iv) or (v); (d) a malate dehydrogenase variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 45 or the mature polypeptide sequence thereof; or (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has malate dehydrogenase activity.

The malate dehydrogenase may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) as described supra. Pyruvate Carboxylases and Polynucleotides Encoding Pyruvate Carboxylases

In some aspects of the recombinant host cells and methods of use thereof, the host cells have pyruvate carboxylase activity. In some aspects, the host cells comprise a heterologous polynucleotide encoding a pyruvate carboxylase. The pyruvate carboxylase can be any pyruvate carboxylase that is suitable for practicing the invention. In one aspect, the pyruvate carboxylase is an enzyme that is present in the cytosol of the host cell.

In one aspect of the recombinant host cells and methods described herein, the pyruvate carboxylase is (a) a pyruvate carboxylase having at least 60% sequence identity to SEQ ID NO: 10 or the mature polypeptide sequence thereof; (b) a pyruvate carboxylase encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii); (c) a pyruvate carboxylase encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, or (vi) the full-length complementary strand of (iv) or (v); (d) a pyruvate carboxylase variant

comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 10 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has pyruvate carboxylase activity.

In one aspect, the pyruvate carboxylase comprises or consists of an amino acid sequence having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% sequence identity to SEQ ID NO: 10, or the mature polypeptide sequence thereof. In one aspect, the pyruvate carboxylase comprises an amino acid sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from SEQ ID NO: 10 or the mature polypeptide sequence thereof.

In one aspect, the pyruvate carboxylase comprises or consists of the amino acid sequence of SEQ ID NO: 10, the mature polypeptide sequence of SEQ ID NO: 10, an allelic variant thereof, or a fragment of the foregoing, having pyruvate carboxylase activity. In another aspect, the pyruvate carboxylase comprises or consists of the amino acid sequence of SEQ ID NO: 10. In another aspect, the pyruvate carboxylase comprises or consists of the mature polypeptide sequence of SEQ ID NO: 10. In another aspect, the pyruvate carboxylase comprises or consists of amino acids 1 to 1193 of SEQ ID NO: 10.

In one aspect, the pyruvate carboxylase is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii) (J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *supra*).

In one aspect, the pyruvate carboxylase is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

In one aspect, the pyruvate carboxylase is encoded by SEQ ID NO: 9 or the mature polypeptide coding sequence thereof. In one aspect, the pyruvate carboxylase is encoded by SEQ ID NO: 9. In one aspect, the pyruvate carboxylase is encoded by the mature polypeptide coding sequence of SEQ ID NO: 9. In one aspect, the pyruvate carboxylase is encoded by a subsequence of SEQ ID NO: 9, wherein the subsequence encodes a polypeptide having pyruvate carboxylase activity. In one aspect, the subsequence contains at least 3060 nucleotides, e.g., at least 3240 nucleotides or at least 3420 nucleotides of SEQ ID NO: 9.

In one aspect, the pyruvate carboxylase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 10, or the mature polypeptide sequence thereof, as described supra. In one aspect, the pyruvate carboxylase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 10. In one aspect, the

pyruvate carboxylase is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 10. In some aspects, the total number of amino acid substitutions, deletions and/or insertions of SEQ ID NO: 10 or the mature polypeptide sequence thereof is not more than 10, e.g., not more than 1, 2, 3, 4, 5, 6, 7, 8 or 9.

In another aspect, the pyruvate carboxylase is a fragment of SEQ ID NO: 10, or the mature polypeptide sequence thereof, wherein the fragment has pyruvate carboxylase activity. In one aspect, the fragment contains at least 1020 amino acid residues, e.g., at least 1080 amino acid residues, or at least 1140 amino acid residues of SEQ ID NO: 10.

The pyruvate carboxylase may also be an allelic variant or artificial variant of a pyruvate carboxylase.

The pyruvate carboxylase can also include fused polypeptides or cleavable fusion polypeptides, as described supra.

The pyruvate carboxylase can also be a variant of a mitochondrial pyruvate carboxylase, such that in vivo importation into the mitochondria is reduced thereby increasing the level of the pyruvate carboxylase variant in the cytosol.

Techniques used to isolate or clone a polynucleotide encoding a pyruvate carboxylase are described supra.

The polynucleotide of SEQ ID NO: 9 or a subsequence thereof, as well as the amino acid sequence of SEQ ID NO: 10 or a fragment thereof, may be used to design nucleic acid probes to identify and clone DNA encoding pyruvate carboxylases from strains of different genera or species, as described supra. Such probes are encompassed by the present invention. A genomic DNA or cDNA library prepared from such other organisms may be screened for DNA that hybridizes with the probes described above and encodes a pyruvate carboxylase, as described supra.

In one aspect, the nucleic acid probe is SEQ ID NO: 9. In another aspect, the nucleic acid probe is the mature polypeptide coding sequence of SEQ ID NO: 9. In another aspect, the nucleic acid probe is a polynucleotide sequence that encodes SEQ ID NO: 10, the mature polypeptide sequence thereof, or a fragment of the foregoing.

For long probes of at least 100 nucleotides in length, very low to very high stringency and washing conditions are defined as described supra. For short probes of about 15 nucleotides to about 70 nucleotides in length, stringency and washing conditions are defined as described supra.

The pyruvate carboxylase may be obtained from microorganisms of any genus. In one aspect, the pyruvate carboxylase may be a bacterial, a yeast, or a filamentous fungal pyruvate carboxylase obtained from the microorganisms described herein. In another aspect, the pyruvate carboxylase is an *Aspergillus oryzae* pyruvate carboxylase, e.g., the *Aspergillus oryzae* pyruvate carboxylase of SEQ ID NO: 10.

Other pyruvate carboxylases that can be used to practice the present invention include, but are not limited to, a *Aspergillus clavatus* NRRL 1 pyruvate carboxylase (XP_001271664; Direct Submission, Submitted (26 Oct. 2006), The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, Md. 20850, USA); *Aspergillus fumigatus* Af293 pyruvate carboxylase (XP_752054; Nierman et al., 2005, *Nature* 438: 1151-1156); *Aspergillus nidulans* FGSC A4 pyruvate carboxylase (XP_662066; Galagan et al., 2005, *Nature* 438: 1105-1115); *Aspergillus niger* pyruvate carboxylase (An15g02820; Pel et al., 2007, *Nature Biotechnology* 25: 221-231; ASPNG 5061; Panne-
man et al., Submitted (July 1998) to the EMBL/GenBank/DBJ databases); *Aspergillus terreus* pyruvate carboxylase

(093918; Direct Submission, Submitted (October 1998) The Institute for Genomic Research, 9712 Medical Center Drive, Rockville, Md. 20850, USA); *Magnaporthe grisea* 70-15 pyruvate carboxylase (XP_367852; Direct Submission, Submitted (26 Sep. 2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, Mass. 02142, USA); *Neurospora crassa* OR74A pyruvate carboxylase (XP_965636; Galagan et al., 2003, *Nature* 422: 859-868); *Rhizopus oryzae* pyruvate carboxylase (RO3G_06931.1); *Saccharomyces cerevisiae* pyruvate carboxylase (NP_009777; Gaffeau et al., 1996, *Science* 274: 546-547); *Schizosaccharomyces pombe* pyruvate carboxylase (NP_595900; Direct Submission, Submitted (29 Jun. 2007) European *Schizosaccharomyces* genome sequencing project, Sanger Institute, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA); and *Ustilago maydis* pyruvate carboxylase (um01054; McCann and Snetselaar, 2008, *Fungal Genetics and Biology* 45: S77-S87). Any aspect described herein related to sequence identity, hybridization, amino acid modifications (e.g., substitutions, deletions, and/or insertions), fragments or subsequences thereof is embraced for the pyruvate carboxylases above.

The pyruvate carboxylase may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) as described supra.

Nucleic Acid Constructs

The present invention also relates to recombinant host cells and methods utilizing nucleic acid constructs comprising a heterologous polynucleotide encoding a bicarbonate transporter (and/or encoding a C4-dicarboxylic acid transporter, a malate dehydrogenase, or a pyruvate carboxylase) linked to one or more (several) control sequences that direct expression in a suitable host cell under conditions compatible with the control sequence(s). Such nucleic acid constructs may be used in any of the host cells and methods describe herein. The polynucleotides described herein may be manipulated in a variety of ways to provide for expression of a desired polypeptide. Manipulation of the polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides utilizing recombinant DNA methods are well known in the art.

The control sequence may be a promoter sequence, a polynucleotide that is recognized by a host cell for expression of a polynucleotide encoding any polypeptide described herein (e.g., a bicarbonate transporter, a C4-dicarboxylic acid transporter, a malate decarboxylase, or a pyruvate carboxylase). The promoter sequence contains transcriptional control sequences that mediate the expression of the polypeptide. The promoter may be any polynucleotide that shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

Each polynucleotide described herein may be operably linked to a promoter that is foreign to the polynucleotide. For example, in one aspect, the heterologous polynucleotide encoding a bicarbonate transporter is operably linked to a promoter that is foreign to the polynucleotide. In another aspect, the heterologous polynucleotide encoding C4-dicarboxylic acid is operably linked to promoter foreign to the polynucleotide. In another aspect, the heterologous polynucleotide encoding a malate dehydrogenase is operably linked to promoter foreign to the polynucleotide. In another

aspect, the heterologous polynucleotide encoding a pyruvate carboxylase is operably linked to promoter foreign to the polynucleotide.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention in a bacterial host cell are the promoters obtained from the *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus subtilis* levansucrase gene (sacB), *Bacillus subtilis* xylA and xylB genes, *E. coli* lac operon, *E. coli* trc promoter (Egon et al., 1988, Gene 69: 301-315), *Streptomyces coelicolor* agarase gene (dagA), and prokaryotic beta-lactamase gene (VIIIa-Kamaroff et al., 1978, *Proc. Natl. Acad. Sci. USA* 75: 3727-3731), as well as the tac promoter (DeBoer et al., 1983, *Proc. Natl. Acad. Sci. USA* 80: 21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Gilbert et al., 1980, *Scientific American*, 242: 74-94; and in Sambrook et al., 1989, *supra*.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Aspergillus oryzae* TAKA amylase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Fusarium oxysporum* trypsin-like protease (WO 96/00787), *Fusarium venenatum* amyloglucosidase (WO 00/56900), *Fusarium venenatum* Daria (WO 00/56900), *Fusarium venenatum* Quinn (WO 00/56900), *Rhizomucor miehei* lipase, *Rhizomucor miehei* aspartic proteinase, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase IV, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* beta-xylosidase, as well as the NA2-tpi promoter (a modified promoter from a gene encoding a neutral alpha-amylase in *Aspergilli* in which the untranslated leader has been replaced by an untranslated leader from a gene encoding triose phosphate isomerase in *Aspergilli*; non-limiting examples include modified promoters from the gene encoding neutral alpha-amylase in *Aspergillus niger* in which the untranslated leader has been replaced by an untranslated leader from the gene encoding triose phosphate isomerase in *Aspergillus nidulans* or *Aspergillus oryzae*); and mutant, truncated, and hybrid promoters thereof.

In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP), *Saccharomyces cerevisiae* triose phosphate isomerase (TPI), *Saccharomyces cerevisiae* metallothionein (CUP1), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos et al., 1992, *Yeast* 8: 423-488.

The control sequence may also be a suitable transcription terminator sequence, which is recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3'-terminus of the polynucleotide encoding the polypeptide. Any terminator that is functional in the host cell of choice may be used in the present invention.

Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase, *Aspergillus oryzae* TAKA amylase, and *Fusarium oxysporum* trypsin-like protease.

Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase (gpd). Other useful terminators for yeast host cells are described by Romanos et al., 1992, *supra*.

The control sequence may also be a suitable leader sequence, when transcribed is a nontranslated region of an mRNA that is important for translation by the host cell. The leader sequence is operably linked to the 5'-terminus of the polynucleotide encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used.

Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

The control sequence may also be a polyadenylation sequence; a sequence operably linked to the 3'-terminus of the polynucleotide and, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence that is functional in the host cell of choice may be used.

Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease, and *Aspergillus niger* alpha-glucosidase.

Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Mol. Cellular Biol.* 15: 5983-5990.

The control sequence may also be a signal peptide coding region that encodes a signal peptide linked to the N-terminus of a polypeptide and directs the polypeptide into the cell's secretory pathway. The 5'-end of the coding sequence of the polynucleotide may inherently contain a signal peptide coding sequence naturally linked in translation reading frame with the segment of the coding sequence that encodes the polypeptide. Alternatively, the 5'-end of the coding sequence may contain a signal peptide coding sequence that is foreign to the coding sequence. The foreign signal peptide coding sequence may be required where the coding sequence does not naturally contain a signal peptide coding sequence. Alternatively, the foreign signal peptide coding sequence may simply replace the natural signal peptide coding sequence in order to enhance secretion of the polypeptide. However, any signal peptide coding sequence that directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used.

Effective signal peptide coding sequences for bacterial host cells are the signal peptide coding sequences obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus licheniformis subtilisin*, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS,

nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

Effective signal peptide coding sequences for filamentous fungal host cells are the signal peptide coding sequences obtained from the genes for *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Aspergillus oryzae* TAKA amylase, *Humicola insolens* cellulase, *Humicola insolens* endoglucanase V, *Humicola lanuginosa* lipase, and *Rhizomucor miehei* aspartic proteinase.

Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding sequences are described by Romanos et al., 1992, *supra*.

The control sequence may also be a propeptide coding sequence that encodes a propeptide positioned at the N-terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to an active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding sequence may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Myceliophthora thermophila* laccase (WO 95/33836), *Rhizomucor miehei* aspartic proteinase, and *Saccharomyces cerevisiae* alpha-factor.

Where both signal peptide and propeptide sequences are present at the N-terminus of a polypeptide, the propeptide sequence is positioned next to the N-terminus of a polypeptide and the signal peptide sequence is positioned next to the N-terminus of the propeptide sequence.

It may also be desirable to add regulatory sequences that allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those that cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the *Aspergillus niger* glucoamylase promoter, *Aspergillus oryzae* TAKA alpha-amylase promoter, and *Aspergillus oryzae* glucoamylase promoter may be used. Other examples of regulatory sequences are those that allow for gene amplification. In eukaryotic systems, these regulatory sequences include the dihydrofolate reductase gene that is amplified in the presence of methotrexate, and the metallothionein genes that are amplified with heavy metals. In these cases, the polynucleotide encoding the polypeptide would be operably linked with the regulatory sequence.

Expression Vectors

The present invention also relates to recombinant host cells and methods utilizing recombinant expression vectors comprising a heterologous polynucleotide encoding a bicarbonate transporter (and/or encoding a C4-dicarboxylic acid transporter, a malate dehydrogenase, or a pyruvate carboxylase); as well as a promoter; and transcriptional and translational stop signals. Such recombinant expression vectors may be used in any of the host cells and methods described herein. The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more (several) convenient restriction sites to allow for insertion or substitution of the polynucleotide encoding the polypeptide at such sites. Alternatively, the polynucleotide(s) may be expressed by inserting the polynucleotide(s) or a nucleic acid construct comprising

the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector may be a linear or closed circular plasmid.

In one aspect, each polynucleotide encoding a bicarbonate transporter, a C4-dicarboxylic acid transporter, a malate dehydrogenase, and/or a pyruvate carboxylase described herein is contained on an independent vector. In one aspect, at least two of the polynucleotides are contained on a single vector. In one aspect, at least three of the polynucleotides are contained on a single vector. In one aspect, all the polynucleotides encoding the bicarbonate transporter, the C4-dicarboxylic acid transporter, the malate dehydrogenase, and the pyruvate carboxylase are contained on a single vector.

The vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the host cell, or a transposon, may be used.

The vector preferably contains one or more (several) selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are the dal genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers that confer antibiotic resistance such as ampicillin, chloramphenicol, kanamycin, or tetracycline resistance. Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, amdS (acetamidase), argB (ornithine carbamoyltransferase), bar (phosphinothricin acetyltransferase), hph (hygromycin phosphotransferase), niaD (nitrate reductase), pyrG (orotidine-5'-phosphate decarboxylase), sC (sulfate adenylyltransferase), and trpC (anthranilate synthase), as well as equivalents thereof. Preferred for use in an *Aspergillus* cell are the amdS and pyrG genes of *Aspergillus nidulans* or *Aspergillus oryzae* and the bar gene of *Streptomyces hygroscopicus*.

The vector preferably contains an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the polynucleotide's sequence encoding the polypeptide or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise

location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term "origin of replication" or "plasmid replicator" means a polynucleotide that enables a plasmid or vector to replicate *in vivo*.

Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM β 1 permitting replication in *Bacillus*.

Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6.

Examples of origins of replication useful in a filamentous fungal cell are AMA1 and ANS1 (Gems et al., 1991, *Gene* 98: 61-67; Cullen et al., 1987, *Nucleic Acids Res.* 15: 9163-9175; WO 00/24883). Isolation of the AMA1 gene and construction of plasmids or vectors comprising the gene can be accomplished according to the methods disclosed in WO 00/24883.

More than one copy of a polynucleotide described herein may be inserted into a host cell to increase production of a polypeptide. An increase in the copy number of the polynucleotide can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the polynucleotide where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the polynucleotide, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, *supra*).

Host Cells

As described herein, the present invention relates to, *inter alia*, recombinant host cells comprising one or more (several) polynucleotide(s) described herein which may be operably linked to one or more (several) control sequences that direct the expression of one or more (several) of the described polypeptides for the recombinant production of a C4-dicarboxylic acid. The invention also embraces methods of using such host cells for the production of a C4-dicarboxylic acid. The host cell may comprise any one or combination of a plurality of the polynucleotides described. For example, in one aspect, the recombinant host cell comprises a heterologous polynucleotide encoding a bicarbonate transporter; and optionally comprises a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter, a heterologous polynucleotide encoding a malate dehydrogenase, and/or a heterologous polynucleotide encoding

pyruvate decarboxylase; wherein the host cell produces (or is capable of producing) a greater amount of a C4-dicarboxylic acid compared to the host cell without the heterologous polynucleotide encoding the bicarbonate transporter when cultivated under the same conditions.

In one aspect, the recombinant host cell comprises:

(1) a heterologous polynucleotide encoding a bicarbonate transporter, such as a C4 bicarbonate transporter selected from: (a) a bicarbonate transporter having at least 60% sequence identity to SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof; (b) a bicarbonate transporter encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii); (c) a bicarbonate transporter encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v); (d) a bicarbonate transporter variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof; and (e) a fragment of (a), (b), (c), or (d) that has bicarbonate transporter activity;

(2) an optional heterologous second polynucleotide encoding a C4-dicarboxylic acid transporter, such as a C4-dicarboxylic acid transporter selected from: (a) a C4-dicarboxylic acid transporter having at least 60% sequence identity to SEQ ID NO: 6 or the mature polypeptide sequence thereof; (b) a C4-dicarboxylic acid transporter encoded by a polynucleotide that hybridizes under low stringency conditions with SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing; (c) a C4-dicarboxylic acid transporter encoded by a polynucleotide having at least 60% sequence identity to SEQ ID NO: 5, the mature polypeptide coding sequence thereof, or the full-length complementary strand of the foregoing; (d) a C4-dicarboxylic acid transporter variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 6 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has C4-dicarboxylic acid transporter activity;

(3) an optional heterologous third polynucleotide encoding a malate dehydrogenase, such as a malate dehydrogenase selected from: (a) a malate dehydrogenase having at least 60% sequence identity to SEQ ID NO: 8 or the mature polypeptide sequence thereof; (b) a malate dehydrogenase encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii); (c) a malate dehydrogenase encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 7 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 7 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v); (d) a malate dehydrogenase variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 8 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has malate dehydrogenase activity; and

(4) an optional heterologous fourth polynucleotide encoding a pyruvate carboxylase, such as a pyruvate carboxylase selected from: (a) a pyruvate carboxylase having at least 60% sequence identity to SEQ ID NO: 10 or the mature polypeptide sequence thereof; (b) a pyruvate carboxylase encoded by a polynucleotide that hybridizes under low stringency conditions with (i) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, or (iii) the full-length complementary strand of (i) or (ii); (c) a pyruvate carboxylase encoded by a polynucleotide having at least 60% sequence identity to (iv) SEQ ID NO: 9 or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 9 or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v); (d) a pyruvate carboxylase variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 10 or the mature polypeptide sequence thereof; and (e) a fragment of a polypeptide of (a), (b), (c), or (d) that has pyruvate carboxylase activity;

wherein the host cell produces (or is capable of producing) a greater amount of a C4-dicarboxylic acid (e.g., malic acid) compared to the host cell without the one or more (several) polynucleotide(s) (e.g., without the heterologous polynucleotide encoding a bicarbonate transporter), when cultivated under the same conditions.

A construct or vector (or multiple constructs or vectors) comprising the one or more (several) polynucleotide(s) is introduced into a host cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source. The aspects described below apply to the host cells, per se, as well as methods using the host cells.

The host cell may be any cell capable of the recombinant production of a polypeptide of the present invention, e.g., a prokaryote or a eukaryote, and/or any cell capable of the recombinant production of a C4-dicarboxylic acid (e.g., malic acid).

The prokaryotic host cell may be any gram-positive or gram-negative bacterium. Gram-positive bacteria include, but not limited to, *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*, *Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*. Gram-negative bacteria include, but not limited to, *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, and *Ureaplasma*.

The bacterial host cell may be any *Bacillus* cell including, but not limited to, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cells.

The bacterial host cell may also be any *Streptococcus* cell including, but not limited to, *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, and *Streptococcus equi* subsp. *Zooepidemicus* cells.

The bacterial host cell may also be any *Streptomyces* cell including, but not limited to, *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, and *Streptomyces lividans* cells.

The introduction of DNA into a *Bacillus* cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Mol. Gen. Genet.* 168: 111-115), by using competent cells (see, e.g., Young and Spizizen, 1961, *J. Bacteriol.* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *J. Mol. Biol.* 56: 209-221), by electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or by conjugation (see, e.g., Koehler and Thorne, 1987, *J. Bacteriol.* 169: 5271-5278). The introduction of DNA into an *E. coli* cell may, for instance, be effected by protoplast transformation (see, e.g., Hanahan, 1983, *J. Mol. Biol.* 166: 557-580) or electroporation (see, e.g., Dower et al., 1988, *Nucleic Acids Res.* 16: 6127-6145). The introduction of DNA into a *Streptomyces* cell may, for instance, be effected by protoplast transformation and electroporation (see, e.g., Gong et al., 2004, *Folia Microbiol. (Praha)* 49: 399-405), by conjugation (see, e.g., Mazodier et al., 1989, *J. Bacteriol.* 171: 3583-3585), or by transduction (see, e.g., Burke et al., 2001, *Proc. Natl. Acad. Sci. USA* 98: 6289-6294). The introduction of DNA into a *Pseudomonas* cell may, for instance, be effected by electroporation (see, e.g., Choi et al., 2006, *J. Microbiol. Methods* 64: 391-397) or by conjugation (see, e.g., Pinedo and Smets, 2005, *Appl. Environ. Microbiol.* 71: 51-57). The introduction of DNA into a *Streptococcus* cell may, for instance, be effected by natural competence (see, e.g., Perry and Kuramitsu, 1981, *Infect. Immun.* 32: 1295-1297), by protoplast transformation (see, e.g., Catt and Jollick, 1991, *Microbios* 68: 189-207), by electroporation (see, e.g., Buckley et al., 1999, *Appl. Environ. Microbiol.* 65: 3800-3804) or by conjugation (see, e.g., Clewell, 1981, *Microbiol. Rev.* 45: 409-436). However, any method known in the art for introducing DNA into a host cell can be used.

The host cell may also be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

The host cell may be a fungal cell. "Fungi" as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota (as defined by Hawksworth et al., *In, Ainsworth and Bisby's Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK) as well as the Oomycota (as cited in Hawksworth et al., 1995, supra, page 171) and all mitosporic fungi (Hawksworth et al., 1995, supra).

The fungal host cell may be a yeast cell. "Yeast" as used herein includes ascosporogenous yeast (Endomycetales), basidiosporogenous yeast, and yeast belonging to the Fungi Imperfecti (Blastomycetes). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in *Biology and Activities of Yeast* (Skinner, F. A., Passmore, S. M., and Davenport, R. R., eds, *Soc. App. Bacteriol. Symposium Series No. 9*, 1980).

The yeast host cell may be a *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* cell such as a *Kluyveromyces lactis*, *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, *Saccharomyces oviformis*, or *Yarrowia lipolytica* cell.

The fungal host cell may be a filamentous fungal cell. "Filamentous fungi" include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth et al., 1995, supra). The filamentous fungi are generally characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevi-*

siae is by budding of a unicellular thallus and carbon catabolism may be fermentative.

The filamentous fungal host cell may be an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocafimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phlebia*, *Piromyces*, *Pleurotus*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Toly-pocladium*, *Trametes*, or *Trichoderma* cell.

For example, the filamentous fungal host cell may be an *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus fumigatus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Bjerkandera adusta*, *Ceriporiopsis aneirina*, *Ceriporiopsis caregiea*, *Ceriporiopsis gilvescens*, *Ceriporiopsis pannocinta*, *Ceriporiopsis rivulosa*, *Ceriporiopsis subrufa*, *Ceriporiopsis subvermispora*, *Chrysosporium inops*, *Chrysosporium keratinophilum*, *Chrysosporium lucknowense*, *Chrysosporium merdarium*, *Chrysosporium pannicola*, *Chrysosporium queenslandicum*, *Chrysosporium tropicum*, *Chrysosporium zonatum*, *Coprinus cinereus*, *Coriolus hirsutus*, *Fusarium bac-tridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Phanerochaete chrysosporium*, *Phlebia radiata*, *Pleurotus eryngii*, *Thielavia terrestris*, *Trametes villosa*, *Trametes versicolor*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* cell.

In one aspect, the host cell is an *Aspergillus* host cell. In another aspect, the host cell is *Aspergillus oryzae*.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known per se. Suitable procedures for transformation of *Aspergillus* and *Trichoderma* host cells are described in EP 238023 and Yelton et al., 1984, *Proc. Natl. Acad. Sci. USA* 81: 1470-1474. Suitable methods for transforming *Fusarium* species are described by Malardier et al., 1989, *Gene* 78: 147-156, and WO 96/00787. Yeast may be transformed using the procedures described by Becker and Guarente, In Abelson, J. N. and Simon, M. I., editors, *Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology*, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito et al., 1983, *J. Bacteriol.* 153: 163; and Hinnen et al., 1978, *Proc. Natl. Acad. Sci. USA* 75: 1920.

In some aspects, the host cell comprises one or more (several) polynucleotide(s) described herein, wherein the host cell secretes (and/or is capable of secreting) an increased level of C4-dicarboxylic acid compared to the host cell without the one or more (several) polynucleotide(s) when cultivated under the same conditions. In some aspects, the host cell secretes and/or is capable of secreting an increased level of C4-dicarboxylic acid (e.g., malic acid) of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the host cell without the one or more (several) polynucleotide(s) (e.g.,

without the heterologous polynucleotide encoding a bicarbonate transporter), when cultivated under the same conditions.

In any of the aspects of the recombinant host cells and methods described herein, the C4-dicarboxylic acid may be malic acid, succinic acid, oxaloacetic acid, malonic acid, or fumaric acid, or combinations thereof. In some aspects, the C4-dicarboxylic acid is malic acid, succinic acid, or fumaric acid, or combinations thereof. In some aspects, the C4-dicarboxylic acid is malic acid or fumaric acid, or a combination of malic acid and fumaric acid. In some aspects, the C4-dicarboxylic acid is malic acid.

In any of these aspects, the host cell produces (and/or is capable of producing) a C4-dicarboxylic acid at a yield of at least 10%, e.g., at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, or at least 90%, of theoretical.

In any of these aspects, the recombinant host has an C4-dicarboxylic acid volumetric productivity (e.g., malic acid volumetric productivity) greater than about 0.1 g/L per hour, e.g., greater than about 0.2 g/L per hour, 0.5 g/L per hour, 0.6 g/L per hour, 0.7 g/L per hour, 0.8 g/L per hour, 0.9 g/L per hour, 1.0 g/L per hour, 1.1 g/L per hour, 1.2 g/L per hour, 1.3 g/L per hour, 1.5 g/L per hour, 1.75 g/L per hour, 2.0 g/L per hour, 2.25 g/L per hour, 2.5 g/L per hour, or 3.0 g/L per hour; or between about 0.1 g/L per hour and about 2.0 g/L per hour, e.g., between about 0.3 g/L per hour and about 1.7 g/L per hour, about 0.5 g/L per hour and about 1.5 g/L per hour, about 0.7 g/L per hour and about 1.3 g/L per hour, about 0.8 g/L per hour and about 1.2 g/L per hour, or about 0.9 g/L per hour and about 1.1 g/L per hour.

The recombinant host cells may be cultivated in a nutrient medium suitable for production of the bicarbonate transporter, C4-dicarboxylic acid transporter, malate dehydrogenase, or pyruvate carboxylase using methods well known in the art. For example, the cell may be cultivated by shake flask cultivation, and small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the desired polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers, may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection), or may be prepared from commercially available ingredients.

The bicarbonate transporter, C4-dicarboxylic acid transporter, malate dehydrogenase, and pyruvate carboxylase, and activities thereof, can be detected using methods known in the art. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. See, for example, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Third Ed., Cold Spring Harbor Laboratory, New York (2001); Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Md. (1999); and Hanai et al., *Appl. Environ. Microbiol.* 73:7814-7818 (2007).

Methods

The present invention also relates to methods of using the recombinant host cells described herein for the production of a C4-dicarboxylic acid. In one aspect, the invention embraces a method of producing a C4-dicarboxylic acid (e.g., malic acid), comprising: (a) cultivating any one of the

recombinant host cells described herein (e.g., any host cell with bicarbonate transporter activity, and optionally, C4-dicarboxylic acid transporter activity, malate dehydrogenase activity, and/or pyruvate carboxylase activity) in a medium under suitable conditions to produce the C4-dicarboxylic acid; and (b) recovering the C4-dicarboxylic acid. In one aspect, the invention embraces a method of producing a C4-dicarboxylic acid (e.g., malic acid), comprising: (a) cultivating in a medium any one of the recombinant host cells described herein, wherein the host cell comprises a heterologous polynucleotide encoding a bicarbonate transporter; and optionally, a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter, a heterologous polynucleotide encoding a malate dehydrogenase, and/or a heterologous polynucleotide encoding a pyruvate decarboxylase under suitable conditions to produce the C4-dicarboxylic acid; and (b) recovering the C4-dicarboxylic acid. In one aspect, the medium is a fermentable medium.

In one aspect of the methods, the C4-dicarboxylic acid (e.g., malic acid) is produced at a titer greater than about 10 g/L, e.g., greater than about 25 g/L, 50 g/L, 75 g/L, 100 g/L, 125 g/L, 150 g/L, 160 g/L, 170 g/L, 180 g/L, 190 g/L, 200 g/L, 210 g/L, 225 g/L, 250 g/L, 275 g/L, 300 g/L, 325 g/L, 350 g/L, 400 g/L, or 500 g/L; or between about 10 g/L and about 500 g/L, e.g., between about 50 g/L and about 350 g/L, about 100 g/L and about 300 g/L, about 150 g/L and about 250 g/L, about 175 g/L and about 225 g/L, or about 190 g/L and about 210 g/L.

In one aspect of the methods, the amount of produced C4-dicarboxylic acid (e.g., malic acid) is at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 50%, or at least 100% greater compared to cultivating the host cell without the polynucleotide that encodes the bicarbonate transporter under the same conditions.

In some aspects of the methods, the C4-dicarboxylic acid is selected from malic acid, succinic acid, oxaloacetic acid, malonic acid, and fumaric acid. In one aspect, the C4-dicarboxylic acid is malic acid.

The recombinant C4-dicarboxylic acid can be optionally recovered from the fermentation medium using any procedure known in the art (see, for example, WO 1998/022611 and U.S. Pat. No. 7,601,865) including, but not limited to, chromatography (e.g., size exclusion chromatography, adsorption chromatography, ion exchange chromatography), electrophoretic procedures, differential solubility, osmosis, distillation, extraction (e.g., liquid-liquid extraction), pervaporation, extractive filtration, membrane filtration, membrane separation, reverse, or ultrafiltration. In one example, the C4-dicarboxylic acid is recovered from other material in the fermentation medium by filtration.

In some aspects of the methods, the recombinant C4-dicarboxylic acid before and/or after being optionally purified is substantially pure. With respect to the methods of producing a C4-dicarboxylic acid (or a specific C4-dicarboxylic acid thereof, such as malic acid), "substantially pure" intends a recovered preparation of the C4-dicarboxylic acid that contains no more than 15% impurity, wherein impurity intends compounds other than C4-dicarboxylic acids. In one variation, a preparation of substantially pure C4-dicarboxylic acid is provided wherein the preparation contains no more than 25% impurity, or no more than 20% impurity, or no more than 10% impurity, or no more than 5% impurity, or no more than 3% impurity, or no more than 1% impurity, or no more than 0.5% impurity.

Suitable assays to test for the production of C4-dicarboxylic acids for the methods of production and host cells

described herein can be performed using methods known in the art. For example, the final C4-dicarboxylic acid product (e.g., malic acid), and other organic compounds, can be analyzed by methods such as HPLC (High Performance Liquid Chromatography), GC-MS (Gas Chromatography-Mass Spectroscopy) and LC-MS (Liquid Chromatography-Mass Spectroscopy) or other suitable analytical methods using routine procedures well known in the art. The release of C4-dicarboxylic acid in the fermentation broth can also be tested with the culture supernatant. Byproducts and residual sugar in the fermentation medium (e.g., glucose) can be quantified by HPLC using, for example, a refractive index detector for glucose and alcohols, and a UV detector for organic acids (Lin et al., *Biotechnol. Bioeng.* 90:775-779 (2005)), or using other suitable assay and detection methods well known in the art.

The present invention is further described by the following examples that should not be construed as limiting the scope of the invention.

EXAMPLES

Chemicals used as buffers and substrates were commercial products of at least reagent grade.

Fungal Strains

Aspergillus oryzae NRRL 3488 (or ATCC 56747) was used as a source of a bicarbonate transporter gene (bt1), a pyruvate carboxylase gene (pyc), a malate dehydrogenase gene (mdh3), and for production of the C4-dicarboxylic acids. *Aspergillus aculeatus* was used as a source of a C4-dicarboxylic acid transport protein gene (c4t521).

Media

YEG medium was composed of 20 g glucose, 5 g yeast extract, and deionized water to 1 liter.

COVE plates were composed of 1 M sucrose, 2% COVE salt solution, 10 mM acetamide, 15 mM CsCl, and 25 g/l Agar Noble.

COVE salt solution was composed of 26 g KCl, 26 g $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 76 g KH_2PO_4 , 50 ml of COVE trace elements solution, and deionized water to 1 liter.

COVE trace elements solution was composed of 0.04 g $\text{Na}_2\text{B}_4\text{O}_7 \cdot 10\text{H}_2\text{O}$, 0.04 g $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$, 1.2 g $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.7 g $\text{MnSO}_4 \cdot \text{H}_2\text{O}$, 0.8 g $\text{Na}_2\text{MoO}_4 \cdot 2\text{H}_2\text{O}$, 10 g $\text{ZnSO}_4 \cdot 7\text{H}_2\text{O}$ and deionized water to 1 liter.

Seed medium was composed of 40 g glucose, 6 g Bacto-peptone, 750 mg KH_2PO_4 , 750 mg K_2HPO_4 , 100 mg $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 100 mg $\text{CaCl}_2 \cdot \text{H}_2\text{O}$, 5 mg $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 5 mg NaCl, and deionized water to 1 liter.

Seed medium B was composed of 30 g glucose, 3 g Bacto-peptone, 560 mg KH_2PO_4 , 560 mg K_2HPO_4 , 925 mg $\text{NaH}_2\text{PO}_4 \cdot \text{H}_2\text{O}$, 820 mg Na_2HPO_4 , 75 mg $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 75 mg $\text{CaCl}_2 \cdot \text{H}_2\text{O}$, 0.75 ml of 1000× Micronutrient Solution, and deionized water to 1 liter.

Acid production medium C was composed of 100 g glucose, 80 g CaCO_3 , 6 g Bacto Peptone, 150 mg KH_2PO_4 , 150 mg K_2HPO_4 , 100 mg $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 100 mg $\text{CaCl}_2 \cdot \text{H}_2\text{O}$, 1 ml 1000× Micronutrient Solution, and deionized water to 1 liter.

Fermentor batch medium was composed of 60 g glucose, 120 g CaCO_3 , 9 g Bacto-peptone, 150 mg KH_2PO_4 , 150 mg K_2HPO_4 , 100 mg $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 100 mg $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 5 mg $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 5 mg NaCl, 5 mL Pluronic L61, and deionized water to 1 liter.

1000× Micronutrient Solution was composed of 5 g NaCl, 5 g $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 1 g citric acid, and deionized water to 1 liter.

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PDA plates were composed of 39 g/l potato dextrose agar. 2XYT+amp plates were composed of 16 g tryptone, 10 g yeast extract, 5 g NaCl, 100 mg ampicillin, 15 g Bacto agar, and deionized water to 1 liter.

Example 1

Cloning of an *Aspergillus oryzae* Bicarbonate
Transporter Gene (bt1) and Construction of
Expression Vector pAmFs69

The bicarbonate transporter gene bt1 (A0090012000782) was cloned from *Aspergillus oryzae* NRRL3488 genomic DNA by PCR amplification using primers homologous to the *Aspergillus oryzae* predicted bicarbonate transporter gene model number A0090012000782 found in the published *A. oryzae* ATCC 42149 genome sequence (Galagan et al., 2005, Nature 438: 1105-1115).

Genomic DNA from *A. oryzae* NRRL3488 was isolated by inoculating 100 ml YEG medium in a shake flask with 2×10^6 spores and incubating the flask at 37° C. overnight with shaking at 200 rpm. The mycelia were harvested in MIRACLOTH® (Calbiochem, San Diego, Calif., USA) lined funnel and approximately 2 grams of tissue was frozen in liquid nitrogen. The mycelia were disrupted by grinding in a cold mortar and pestle. Genomic DNA was isolated from the powdered mycelia using a DNeasy® Plant Maxi Kit (QIAGEN Inc., Valencia, Calif., USA) according to the manufacturer's instructions. The *Aspergillus oryzae* bt1 gene was amplified using forward primer 069824 and reverse primer 069825 shown below:

Primer 069824:

(SEQ ID NO: 11)
5'-GTGATAGAACATCGTCCATAATGGAATCCAGCGCTGTACA-3'

Primer 069825:

(SEQ ID NO: 12)
5'-GTGTCAGTCACCTCTAGTTATCAGATTCAATCTCGTCTT-3'

The amplification reactions were performed using Phusion® Hot Start High-Fidelity DNA Polymerase (Finnzymes OY, Finland) according to manufacturer's instructions. Each PCR reaction contained 47 ng of *Aspergillus oryzae* NRRL3488 genomic DNA, 200 µM dNTPs, 50 pM of forward primer, 50 pM reverse primer, 1× Phusion® GC Buffer reaction buffer (Finnzymes OY, Finland), and 50 units of Phusion® Hot Start High-Fidelity DNA Polymerase in a final volume of 50 µl. The amplification reactions were incubated in an EPPENDORF® MASTERCYCLER® (Eppendorf Scientific Inc., Westbury, N.Y., USA) programmed for 1 cycle at 98° C. for 30 seconds; 35 cycles at 98° C. for 10 seconds, 66° C. for 30 seconds, and 72° C. for 2.5 minutes; and 1 cycle at 72° C. for 10 minutes. The PCR product was purified by 1% agarose gel electrophoresis in 50 mM Tris base-50 mM acetate-0.1 mM disodium EDTA (TAE) buffer. A fragment of approximately 2.5 kb was excised from the gel and extracted from the agarose using a QIAQUICK® Gel Extraction Kit (QIAGEN Inc., Valencia, Calif., USA).

Plasmid pShTh60 (FIG. 1; see also PCT Application No. PCT/US10/47002, filed Aug. 27, 2010) was digested with Sex AI and Pac I, separated by 0.8% agarose gel electrophoresis in TBE buffer (10.8 g/L Tris Base, 5.5 g/L Boric acid, 2 mM EDTA, pH 8.0) and purified using a QIAQUICK® Gel Extraction Kit (QIAGEN Inc., Valencia, Calif., USA). The purified PCR product above was then

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inserted into the digested pShTh60 fragment using an In-Fusion™ Advantage reaction kit (Clontech, Mountain View, Calif., USA) according to the manufacturer's instructions resulting in plasmid pAmFs69 (FIG. 2).

A 2.5 µl aliquot of the ligation reaction above was transformed into ONE SHOT® TOP10 chemically competent *E. coli* cells according to the manufacturer's instructions. Transformants were plated onto 2XYT+amp plates and incubated at 37° C. overnight.

DNA sequence analysis was used on the resulting transformants to confirm the integrity of the bt1 coding sequence. Primers 610849, 610851, 610853, 610855, 610857, 610859, and 610861 shown below were used with an ABI3130XL DNA Analyzer (Applied Biosystems, Inc., Foster City, Calif., USA) and the primer walking technique with dye-terminator chemistry (Giesecke et al., 1992, *J. Virol. Methods* 38: 47-60).

(SEQ ID NO: 13)
Primer 610849: 5'-GAACAGGAAGAAATCCAAAA-3'

(SEQ ID NO: 14)
Primer 610851: 5'-GTCGCATAGCCACTGCAAT-3'

(SEQ ID NO: 15)
Primer 610853: 5'-TGTTGCCGCCAAGGGACTTA-3'

(SEQ ID NO: 16)
Primer 610855: 5'-CCGAGAGCGTTGAGTTAATC-3'

(SEQ ID NO: 17)
Primer 610857: 5'-AGCATTAGGGCTAGTCCGT-3'

(SEQ ID NO: 18)
Primer 610859: 5'-CCAAGATGCCATGTCAGGAC-3'

(SEQ ID NO: 19)
Primer 610861: 5'-TCACAAAAGAGTAGAGGCCA-3'

The nucleotide construct of the genomic DNA sequence (SEQ ID NO: 1), and deduced amino acid sequence (SEQ ID NO: 2) of the *Aspergillus oryzae* bt1 gene are shown in FIGS. 3A and 3B. The genomic coding sequence of 2503 bp (including one stop codon) is interrupted by three introns of 78 bp (465-542), 51 bp (1173-1223), and 61 bp (1747-1807). The corresponding cDNA sequence (bold nucleotide sequence shown in FIGS. 3A and 3B) is 2313 bp, including one stop codon. The predicted encoded protein is 770 amino acids, with a predicted molecular mass of 83.9 kDa and an isoelectric pH of 6.9.

Example 2

Cloning of an *Aspergillus oryzae* Bicarbonate
Transporter Gene AO090003000798 and
Construction of Corresponding Expression Vector

The bicarbonate transporter gene bt2 (AO090003000798) was cloned from *Aspergillus oryzae* NRRL3488 genomic DNA by PCR amplification using primers homologous to the *Aspergillus oryzae* predicted bicarbonate transporter gene model number AO090003000798 found in the published *A. oryzae* ATCC 42149 genome sequence (Galagan et al., 2005, supra).

Genomic DNA from *A. oryzae* NRRL3488 was isolated and the mycelia were harvested and processed as described in Example 1. The *Aspergillus oryzae* bt2 gene was amplified using forward primer 0614058 and reverse primer 0614057 shown below:

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Primer 0614058:

(SEQ ID NO: 52)

5'-GTGATAGAACATCGTCCATAATGCCGGCGATCTCAAAACC-3'

Primer 0614057:

(SEQ ID NO: 53)

5'-GTGTGAGTCACCTCTAGTTACTATGCATCAAGGACATTC-3'

The amplification reactions were performed using Phusion® Hot Start High-Fidelity DNA Polymerase (Finnzymes) according to manufacturer's instructions. Each PCR reaction contained 47 ng of *Aspergillus oryzae* NRRL3488 genomic DNA, 200 µM dNTPs, 50 pM of forward primer, 50 pM reverse primer, 1× Phusion® GC Buffer reaction buffer (Finnzymes), and 50 units of Phusion® Hot Start High-Fidelity DNA Polymerase in a final volume of 50 µl. The amplification reactions were incubated in an EPPENDORF® MASTERCYCLER® (Eppendorf Scientific Inc.) programmed for 1 cycle at 98° C. for 2 minutes; 35 cycles at 98° C. for 15 seconds, 65° C. for 15 seconds, and 74° C. for 1 minute; and 1 cycle at 74° C. for 1 minute. The PCR product was purified by 1% agarose gel electrophoresis in 50 mM Tris base-50 mM acetate-0.1 mM disodium EDTA (TAE) buffer. A fragment of approximately 2.7 kb was excised from the gel and extracted from the agarose using a QIAQUICK® Gel Extraction Kit (QIAGEN Inc.).

Plasmid pShTh77 (FIG. 11) was digested with Sex AI and Pac I, separated by 0.8% agarose gel electrophoresis in TBE buffer (10.8 g/L Tris Base, 5.5 g/L Boric acid, 2 mM EDTA, pH 8.0) and purified using a QIAQUICK® Gel Extraction Kit (QIAGEN Inc., Valencia, Calif., USA). The purified PCR product above was then inserted into the digested pShTh77 fragment using an In-Fusion™ Advantage reaction kit (Clontech) according to the manufacturer's instructions resulting in plasmid pShTh147 (FIG. 12).

A 2.5 µl aliquot of the ligation reaction above was transformed into ONE SHOT® TOP10 chemically competent *E. coli* cells according to the manufacturer's instructions. Transformants were plated onto 2XYT+amp plates and incubated at 37° C. overnight.

DNA sequence analysis was used on the resulting transformants to confirm the integrity of the bt2 coding sequence. Primers 0614313, 0614314, 996270, and 0611428, shown below were used with an ABI3130XL DNA Analyzer (Applied Biosystems, Inc., Foster City, Calif., USA) and the primer walking technique with dye-terminator chemistry (Giesecke et al., 1992, *J. Virol. Methods* 38: 47-60).

(SEQ ID NO: 54)

Primer 0614313: 5'-GATTGAGATCGGCATTACT-3'

(SEQ ID NO: 55)

Primer 0614314: 5'-ACGCGGAACAGCAGAATGGC-3'

(SEQ ID NO: 56)

Primer 996270: 5'-CTATAGCGAAATGGATTGTTGTCT-3'

(SEQ ID NO: 57)

Primer 0611428: 5'-TTCACCGTGAACGTATTGA-3'

The nucleotide construct of the genomic DNA sequence (SEQ ID NO: 3), and deduced amino acid sequence (SEQ ID NO: 4) of the *Aspergillus oryzae* bt1 gene are shown in FIGS. 4A and 4B. The genomic coding sequence of 2657 bp (including stop codon) is interrupted by two introns of 64 bp (302-365) and 61 bp (512-572). The corresponding cDNA sequence (bold nucleotide sequence shown in FIGS. 4A and 4B) is 2532 bp, including one stop codon. The predicted

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encoded protein is 843 amino acids, with a predicted molecular mass of 92.5 kDa and an isoelectric pH of 8.4.

Example 3

Cloning of an *Aspergillus aculeatus* C4-Dicarboxylic Acid Transporter Gene and Construction of Expression Vector pSaMF36

Genomic DNA from *Aspergillus aculeatus* was isolated by inoculating 100 ml of YEG medium in a shake flask with 2×10^6 spores and incubating the flask at 34° C. overnight with shaking at 160 rpm. The mycelia were harvested by filtration using a MIRACLOTH® (Calbiochem, San Diego, Calif., USA) lined funnel and approximately 2 g of mycelia were recovered and frozen in liquid nitrogen. The frozen mycelia were disrupted by quickly smashing with a hammer while wrapped inside the MIRACLOTH®. The disrupted mycelia were then transferred to a 50 ml polypropylene conical centrifuge tube containing 10 ml of 1× lysis buffer (100 mM EDTA, 10 mM Tris pH 8.0, 1% Triton® X-100, 0.5 M Guanidine-HCl, 200 mM NaCl) and 3 µl of RNase A (QIAGEN Inc., Valencia, Calif., USA, 100 mg/ml). The tube was mixed by gentle vortexing, and then incubated at room temperature for 5 minutes after which was added 150 µl Proteinase K (QIAGEN Inc., Valencia, Calif., USA; 20 mg/ml). The tube was mixed by inversion and incubated at 50° C. for 1 hour. The tube was then centrifuged at 7240×g for 20 minutes. The supernatant was then added to a pre-equilibrated QIAGEN-tip 100 (QIAGEN Inc., Valencia, Calif., USA) and the remaining DNA extraction steps were performed according to the manufacturer's instructions. The DNA was resuspended in 100 µl TE buffer (10 mM Tris Base, 1 mM EDTA, pH 8.0).

The 1257 bp C4-dicarboxylic acid transporter gene c4t521 was amplified from isolated *Aspergillus aculeatus* genomic DNA using primers 069700 and 069701 shown below.

Primer 069700:

(SEQ ID NO: 20)

5'-TGTGATAGAACATCGTCCATAATGCACGACCACAGC-3'

Primer 069701:

(SEQ ID NO: 21)

5'-GTGTGAGTCACCTCTAGTTATCATTCGAACAACCTCGGACA-3'

The PCR reaction was composed of 10 µl 5× reaction buffer, 1 µl *A. aculeatus* genomic DNA template (105 ng/µl), 1 µl primer 069700 (100 ng/µl), 1 µl primer 069701 (100 ng/µl), 1 µl dNTP mixture (10 mM), 35.5 µl deionized water, and 0.5 µl Phusion™ Hot Start High-Fidelity DNA polymerase (Finnzymes, Inc., Massachusetts, USA). The amplification reaction was incubated in an EPPENDORF® MASTERCYCLER® programmed for 1 cycle at 98° C. for 30 seconds; 30 cycles each at 98° C. for 10 seconds, 60° C. for 30 seconds, 72° C. for 1 minute; and one cycle at 72° C. for 10 minutes. The PCR product was digested with Dpn I for 1 hour to degrade any plasmid DNA template.

Plasmid pShTh60 (FIG. 1) was digested with Sex AI and Pac I, separated by 0.8% agarose gel electrophoresis in TBE buffer, and purified using a QIAQUICK® Gel Extraction Kit. The purified PCR product above was then inserted into the digested pShTh60 fragment using an In-Fusion™ Advantage reaction kit composed of 2 µl 5× buffer, 3 µl purified PCR product (26 ng/µl), 1.5 µl gel-purified Sex AI and Pac I digested and gel-purified pShTh60 (132 ng/µl), 1

μl In-Fusion™ enzyme and 2.5 μl deionized water. The reaction was incubated at 37° C. for 15 minutes, 50° C. for 15 minutes, placed on ice for 5 minutes and diluted with 40 μl TE buffer resulting in pSaMF36 (FIG. 5).

A 2.5 μl aliquot of the ligation reaction above was transformed into ONE SHOT® TOP10 chemically competent *E. coli* cells according to the manufacturer's instructions. Transformants were plated onto 2XYT+amp plates and incubated at 37° C. overnight. The resulting transformants were picked and subjected to DNA sequencing to confirm that the mat521 gene was successfully integrated into the vector.

The nucleotide construct of the genomic DNA sequence (SEQ ID NO: 5) and deduced amino acid sequence (SEQ ID NO: 6) of the *Aspergillus aculeatus* c4t521 gene are shown in FIG. 6. The genomic coding sequence of 1257 bp (including stop codon) contains no introns. The predicted encoded protein is 418 amino acids, with a predicted molecular mass of 46.8 kDa and an isoelectric pH of 6.36. Using the SignalP program (Nielsen et al., 1997, *Protein Engineering* 10:1-6), a signal peptide of 17 residues was predicted. Based on this program, the predicted mature protein contains 401 amino acids with a predicted molecular mass of 44.9 kDa and an isoelectric pH of 6.89.

Example 4

Cloning of an *Aspergillus oryzae* Malate Dehydrogenase Gene and Construction of Expression Vector pSaMF21

Plasmid pSaMF21 was constructed to contain the NAD-dependent malate dehydrogenase (mdh3) gene sequence (DOGAN: AO090701000013), a 1430 bp fragment from *Aspergillus oryzae* as described in PCT Application No. PCT/US10/47002, filed Aug. 27, 2010. The nucleotide construct of the genomic DNA sequence (SEQ ID NO: 7) and deduced amino acid sequence (SEQ ID NO: 8) of the *Aspergillus oryzae* NRRL 3488 malate dehydrogenase mdh3 gene are shown in FIG. 7. The genomic coding sequence of 1430 bp (including stop codon) is interrupted by 7 introns of 57 bp (14-70 bp), 70 bp (103-172 bp), 74 bp (284-357 bp), 68 bp (446-513 bp), 58 bp (892-949 bp), 48 bp (1035-1082 bp), and 62 bp (1228-1289 bp). The G+C content of the coding region of the mdh3 gene is 50.3%. The corresponding cDNA sequence (bold nucleotide sequence shown in FIG. 7) is 993 bp, including one stop codon. The predicted encoded protein is 330 amino acids with a predicted mass of 34.5 kDa and an isoelectric pH of 6.79.

Briefly, the plasmid was constructed by linearizing pShTh60 (FIG. 1) by restriction digestion with Sex AI and Pac I. The digested vector was separated by 0.8% agarose gel electrophoresis in TBE buffer and purified using a QIAQUICK® Gel Extraction Kit. The mdh3 gene was amplified from pShTh71 (PCT Application No. PCT/US10/47002, filed Aug. 27, 2010) using primers 067522 and 067525.

Primer 067522:

(SEQ ID NO: 22)
5'-AGAACATCGTCCATAATGGTCAAAGCTGGTGAGTTA-3'

Primer 067525:

(SEQ ID NO: 23)
5'-GTGTCAGTCACCTCTAGTTATTACTTTGGTGGTGGTTCT-3'

The PCR reaction was composed of 5 μl 10× reaction buffer, 1 μl pShTh71 template (87 ng/μl), 1 μl primer 067522 (100 ng/μl), 1 μl primer 067525 (100 ng/μl), 1 μl dNTP mixture (10 mM), 45.5 μl deionized water, and 0.5 μl Herculase® HotStart DNA polymerase (Stratagene, La Jolla, Calif., USA). The amplification reaction was incubated in an EPPENDORF® MASTERCYCLER® programmed for 1 cycle at 95° C. for 2 minutes; 10 cycles each at 95° C. for 10 seconds, 58° C. for 30 seconds, and 72° C. for 1.5 minutes; 20 cycles each at 95° C. for 10 seconds, 50° C. for 30 seconds, and 72° C. for 1.5 minutes plus 10 seconds per cycle. The PCR reaction was subjected to a restriction digest with Dpn I for 1 hour to degrade any plasmid DNA template. The PCR product was then purified using the MinElute® PCR Purification Kit (QIAGEN Inc., Valencia, Calif., USA). The purified PCR product was inserted into the vector using an In-Fusion™ Advantage reaction composed of 2 μl 5× buffer, 0.5 μl purified PCR product (110 ng/μl), 1.7 μl gel-purified Sex AI and Pac I restriction digested pShTh60 (FIG. 1; 78 ng/μl), 1 μl In-Fusion™ enzyme and 4.8 μl deionized water. The reaction was incubated at 37° C. for 15 minutes followed by 50° C. for 15 minutes after which it was placed on ice for 5 minutes and diluted with 40 μl TE buffer resulting in pSaMF21 (FIG. 8). A 2 μl aliquot of the ligation reaction was transformed into ONE SHOT® TOP10 chemically competent *E. coli* cells (Invitrogen, San Diego, Calif., USA) according to the manufacturer's instructions. Transformants were plated onto 2XYT+amp plates and incubated at 37° C. overnight. The resulting transformants were picked and subjected to DNA sequencing to confirm that the mdh3 gene was successfully integrated into the vector.

Example 5

Cloning of an *Aspergillus oryzae* Pyruvate Carboxylase Gene and Construction of Expression Vector pRyan1

Plasmid pRyan1 was constructed to contain the pyruvate carboxylase (pyc) gene sequence (DOGAN: AO090023000801), a 3646 bp fragment from *Aspergillus oryzae* (including two stop codons) as described in PCT Application No. PCT/US10/47002, filed Aug. 27, 2010. The nucleotide construct of the genomic DNA sequence (SEQ ID NO: 9) and deduced amino acid sequence (SEQ ID NO: 10) of the *Aspergillus oryzae* pyruvate carboxylase gene are shown in FIGS. 9A and 9B. Both the *Aspergillus oryzae* NRRL 3488 and ATCC 56747 pyruvate carboxylase genes have the same nucleotide sequence. The G+C content of the coding region of the gene is 57.1%. The genomic coding sequence of 3643 bp (including one stop codon) is interrupted by 1 intron of 61 bp (3475-3535 bp). The G+C content of the coding region of the gene is 57.1%. The corresponding cDNA sequence (bold nucleotide sequence shown in FIGS. 9A and 9B) is 3582 bp, including one stop codon. The predicted encoded protein is 1193 amino acids with a predicted mass of 131 kDa.

Briefly, the plasmid was constructed by linearizing pShTh60 (FIG. 1) by restriction digestion with Sex AI and Pac I. The digested vector was separated by 0.8% agarose gel electrophoresis in TBE buffer and purified using a

QIAQUICK® Gel Extraction Kit. The pyc gene was amplified from *Aspergillus oryzae* NRRL 3488 genomic DNA using primers 066549 and 067388 shown below.

Primer 066549: (SEQ ID NO: 24)
5'-TAGAACATCGTCCATAATGGCGGCTCCGTTTCGTCA-3'

Primer 067388: (SEQ ID NO: 25)
5'-GTGTCAGTCACCTCTAGTTATTATTACGCTTTGACGATCT-3'

The PCR reaction was composed of 5 µl 10× reaction buffer, 1 µl *Aspergillus oryzae* NRRL3488 genomic DNA (110 ng/µl), 1 µl primer 066549 (100 ng/µl), 1 µl primer 067388 (100 ng/µl), 1 µl dNTP mixture (10 mM), 45.5 µl deionized water, and 0.5 µl Herculase® HotStart DNA polymerase. The amplification reaction was incubated in an EPPENDORF® MASTERCYCLER® programmed for 1 cycle at 95° C. for 2 minutes; 10 cycles each at 95° C. for 10 seconds, 58° C. for 30 seconds, and 72° C. for 3.5 minutes; 20 cycles each at 95° C. for 10 seconds, 58° C. for 30 seconds, and 72° C. for 3.5 minutes plus 10 seconds per cycle. The PCR product was then purified using a MinElute® PCR Purification Kit.

The purified PCR product was inserted into the vector using an In-Fusion™ Advantage reaction composed of 2 µl 5× buffer, 1 µl purified PCR product (144 ng/µl), 2 µl gel purified Sex AI and Pac I restriction digested pShTh60 (FIG. 1; 78 ng/µl), 1 µl In-Fusion™ enzyme and 4 µl deionized water. The reaction was incubated at 37° C. for 15 minutes followed by 50° C. for 15 minutes after which it was placed on ice for 5 minutes and diluted with 40 µl TE buffer resulting in pRYAN1 (FIG. 10). A 2 µl aliquot of the ligation reaction was transformed into ONE SHOT® TOP10 chemically competent *E. coli* cells according to the manufacturer's instructions. Transformants were plated onto 2XYT+amp plates and incubated at 37° C. overnight. The resulting transformants were picked and subjected to DNA sequencing to confirm that the pyc gene was successfully integrated into the vector. Nucleotide 1308 was changed from C to T, but did not affect the protein sequence.

Example 6

Transformation of Expression Vector Fragments of pAmFs69, pRyan1, pSaMf21, pSaMf36 into *Aspergillus oryzae* NRRL3488 (ShTh6900)

Protoplast preparation and transformation of *Aspergillus oryzae* NRRL3488 were performed by inoculating approximately 2×10^7 spores into 100 ml YEG medium and incubating the flask at 27° C. for 16-18 hours at 140 rpm. Mycelia were collected by pouring the culture through a sterile funnel lined with MIRACLOTH® and rinsing with 50 ml of 0.7 M KCl. The washed mycelia were resuspended in a 125 ml flask with 20 ml of protoplasting solution composed of 5 mg of GLUCANEX™ (Novozymes NS, Bagsværd, Denmark) and 0.5 mg of chitinase (Sigma, USA) per ml of 0.7 M KCl (filter sterilized) and incubated at 34° C., for 30 minutes with mixing at 80 rpm. The protoplasting solution was poured through a sterile funnel lined with MIRACLOTH® and rinsed with 50 ml of STC composed of 1 M sorbitol-10 mM Tris-HCl pH 6.5-10 mM CaCl₂. The flow-through was collected in two 50 ml polypropylene tubes. The tubes were spun in the centrifuge at 1300×g for 10 minutes at room temperature. The supernatant was dis-

carded and the protoplast pellet was resuspended in 20 ml of STC buffer. The protoplasts were washed by two rounds pellet resuspension in 20 ml of STC buffer and centrifugation at 1300×g for 10 minutes at room temperature. The final pellet was resuspended in 2 ml of STC buffer. The protoplasts were counted by removing a 10 µl sample and counting them in a haemocytometer (VWR, West Chester, Pa., USA). The volume was adjusted with STC buffer to obtain a protoplast concentration of 2×10^7 per ml.

The plasmid expression vectors pAmFs69 (Example 1), pSaMf36 (Example 3), pSaMf21 (Example 4) and pRyan1 (Example 5) were individually prepared for transformation by restriction digestion with Pme I for 4 hours at 37° C. The approximately 5-6 kb expression cassettes from each construct were separated from the vector sequences by 0.8% agarose gel electrophoresis in TBE buffer, and purified using a QIAQUICK® Gel Extraction Kit according to manufacturer's instructions.

Four transformation reactions were prepared by adding 100 µl of protoplast preparation above into four 12 ml polypropylene tubes. To each tube was added two micrograms of the digested pRyan1 pyc fragment, and one microgram each of the digested pAmFs69 bt1 fragment, digested pSaMf36 C4T521 fragment, and the digested pSaMf21 mdh fragment to a 250 µl polyethylene glycol (PEG) solution (60% w/v polyethylene glycol (PEG), 10 mM Tris 6.5, mM CaCl) followed by gentle mixing and incubation at 37° C. for 30 minutes. Each transformation reaction was diluted with 6 ml of STC buffer, followed by plating three separate aliquots onto COVE plates. Each plate was then incubated at 34° C. for 7-10 days. Sixty of the resulting transformants (designated ShTh6900 transformants) were transferred to individual COVE plates and incubated at 34° C. for 5 days. Spore stocks were prepared by collecting the spores in 0.1% TWEEN® 80. Cultures were stored by preparing a glycerol stock of each (800 µl spore stock, 200 µl 0.1% TWEEN® 80) and frozen at -80° C.

Transformants were grown in shake flask and genomic DNA isolated according to the description above. Individual PCR reactions to test for the presence of each of the four expression vector fragments were composed of 5 µl 10× reaction buffer; 0.5 µl template (80-300 ng/µl); 1.0 µl forward primer (50 pM; see below); 1.0 µl reverse primer (50 pM; see below); 0.5 µl dNTP mixture (10 mM), 16.75 µl deionized water, and 0.25 µl Phusion® DNA polymerase.

Forward Primer 065067 (for the pRyan1 pyc, pSaMf21 mdh, and pSaMf36 C4T521 fragments):

(SEQ ID NO: 46)
5'-TGACCTTCCACGCTGACCAC-3'

Forward Primer 0610854 (for the pAmFs69 bt1 fragment):

(SEQ ID NO: 47)
5'-GGCTGAGAAAATATGTTGCA-3'

Reverse Primer 0611365 (for the pSaMf36 C4T521 fragment):

(SEQ ID NO: 48)
5'-GATAGACCACTAATCATGGTGGCGATGGAG-3'

Reverse Primer 061752 (for the pRyan1 pyc fragment)

(SEQ ID NO: 49)
5'-TGCGGTCCTGAGTCAGGCCAGTTGCTCGA-3'

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-continued

Reverse Primer 062400 (for the pSaMF21 mdh fragment)

5'-GGGATTGAACAGCAGAAGG-3' (SEQ ID NO: 50)

Reverse Primer 996270 (for the pAmFs69 bt1 fragment)

5'-TCACAAAAGAGTAGAGGCCA-3' (SEQ ID NO: 51)

The amplification reactions were incubated in an EPPENDORF® MASTERCYCLER® programmed for 1 cycle at 98° C. for 30 seconds; 35 cycles each at 98° C. for 10 seconds; 66° C. (for the pRyan1 pyc fragment) or 58° C. (for the pAmFs69 bt1, pSaMF21 mdh, and pSaMF36 C4T521 fragments) for 10 seconds; 72° C. for 15 seconds; and one cycle of 72° C. for 10 minutes. *Aspergillus oryzae* NRRL 3488 genomic DNA (110 ng/μl) was used as a negative control template and each plasmid (pRyan1, pAmFs69, pSaMF21, or pSaMF36 diluted to 20 ng/μl) was used as positive control template. Amplification reaction mixtures were analyzed by gel electrophoresis using 2 μl of each reaction mixture on a 0.8% agarose gel. Transformants resulting in the expected PCR fragment sizes confirming integration were then tested for production of malic acid as described below.

Control transformants containing expression vector fragments of pSaMF36, pSaMF21, and pRyan1, but lacking pAmFs69 (designated SaMF3603 transformants) were prepared and verified in a similar procedure to that described above.

Example 7

Production of Malic Acid in Shake Flask Cultures of *Aspergillus oryzae* Transformants Containing Expression Vector Fragments of pAmFs69, pRyan1, pSaMF21, and pSaMF36 (ShTh6900)

Spores from ShTh6900 transformants described in Example 6 and *Aspergillus oryzae* NRRL 3488 as a control were plated onto individual PDA plates and allowed to sporulate at 34° C. for 5 to 7 days. Spores were collected in 0.1% TWEEN® 80 and counted using a hemacytometer. Seed cultures were prepared in 250 ml flasks containing 100 ml of seed medium B and inoculated with 300 μl of spore suspension. Seed cultures were grown for approximately 17 hours at 30° C. with shaking at 200 rpm. Acid production cultures were prepared in 250 ml unbaffled flasks containing 50 ml of acid production medium C and 3 ml of the 17 hour seed cultures. Cultures were incubated at 30° C. with shaking at 200 rpm for 2-10 days.

Quantitation of malic acid for the shake flask culture transformants was performed by Reverse Phase High Pressure Liquid Chromatography (RP-HPLC) using an 1200 Series Binary LC System and 1200 Series Diode Array Detector (DAD) (Agilent Technologies, Santa Clara, Calif. USA). Reverse phase separation was performed using an Aqua 5μ C18 125 Å 205×4.6 mm ID column and AQ C18 4×3.0 mm Security Guard Cartridge (Phenomenex, Inc., Torrance, Calif., USA). The mobile phase consisted of 10% methanol (HPLC grade) and 90% 145 mM phosphate pH 1.5 buffer.

Whole culture samples were removed and diluted 1:10 in HPLC Running Buffer composed of 850 ml of 64 mM phosphate buffer and 150 ml of methanol pH 1.65. The samples were then filtered through a 25 mm 0.45 micron

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polyethersulfone membrane (Whatman, Florham Park, N.J., USA) and 1.5 ml of the filtrates were placed into a HPLC vial for acid analysis. The remaining amount of the shake flask cultures were filtered through 3 layers of cheese cloth and rinsed three times with 10 volumes of double distilled sterile water to remove insoluble CaCO₃. Cell pellets were harvested from the cheese cloth, placed into a 15 ml culture tube and stored at -20° C.

RP-HPLC was performed using an injection volume of 10 μl at a flow rate of 0.7 ml/minute (isocratic) with a column temperature of 25° C. and run time of 11 minutes. Detection was set at 210 nm, 8 nm bandwidth, with the reference at 360 nm, 40 nm bandwidth. The void time was determined to be 3.8 minutes. The quantitative capabilities of the reverse phase method were determined for malic acid by performing replicate injections of serially diluted malic acid standards with concentrations ranging from 49.2-3.93 mM. The relative standard deviation for (RSD) for replicate injections was 5%. Malic acid shows R²≥0.9999.

Aspergillus oryzae ShTh6900 transformants containing expression vector fragments of pAmFs69, pRyan1, pSaMF21, and pSaMF36 showed malic acid titers more than two-fold over the *Aspergillus oryzae* NRRL 3488 control strains, and higher than titers observed in separate experiments with SaMF3603 transformants (containing expression vector fragments of pSaMF36, pSaMF21, and pRyan1, but lacking the expression vector fragment of pAmFs69).

Example 8

Fermentation of *Aspergillus oryzae* Transformants Containing Expression Vector Fragments of pAmFs69, pRyan1, pSaMF21, and pSaMF36 (ShTh6900)

Aspergillus oryzae ShTh6900 transformants described in Example 7 and control transformant *Aspergillus oryzae* SaMF3603 (containing expression vector fragments of pSaMF36, pSaMF21, and pRyan1, but lacking the expression vector fragment of pAmFs69) were grown for approximately 7 days at 34° C. on PDA plates. A 5-6 ml volume of sterile sodium phosphate buffer (50 mM, pH 6.8) containing 0.2% TWEEN® 80 was added to each plate and spores were suspended by scraping with an inoculating loop. Each suspension was transferred by pipette to a 50 ml conical tube. For each tube, 25 ml of sterile sodium phosphate buffer (50 mM, pH 6.8) containing 0.2% TWEEN® 80 was added to a 500 ml unbaffled flask containing 75 ml of seed medium, which was then inoculated with 2 ml of spore suspension. The flasks were then incubated at 34° C. and 180 rpm for about 24 hours. The seed flasks were combined to supply the 144 ml inoculum required per tank.

Three-liter fermentors containing 1.8 liters of fermentor batch medium were individually inoculated by introducing 144 ml (8%) of the seed culture broth from three combined seed flasks of either an *Aspergillus oryzae* ShTh6900 transformants or an *Aspergillus oryzae* ShTh3603 transformants. The fermentors were equilibrated at 34° C. ±0.1° C. and stirred at 500 rpm. Inlet air flow was maintained at 1 v/v/m. A 25% glucose stream was administered at a rate of approximately 7.3 g/hr beginning at about 20 hours of fermentation. Sterile CaCO₃ (about 100 g) was added around day 5 to keep the fermentation pH in the range of 6 to 7. Samples were withdrawn daily and analyzed for malic acid production as described in Example 6. Fermentation was completed after 7 or 8 days.

The ShTh6900 transformants showed higher malic acid titers than the SaMF3603 control strains, with a faster production rate (especially over the first 72 hours) and a more rapid consumption of glucose.

Example 9

Transformation of Expression Vector Fragments of pShTh147 into *Aspergillus oryzae* M727 (ShTh147)

Protoplast preparation and transformation of *Aspergillus oryzae* M727 (a mutant strain of ShTh6900 produced by standard mutagenesis with NTG and selected for increased C4 acid production) were performed by inoculating approximately 2×10^7 spores into 100 ml YEG medium and incubating the flask at 27° C. for 16-18 hours at 140 rpm. Mycelia were collected by pouring the culture through a sterile funnel lined with MIRACLOTH® and rinsing with 50 ml of 0.7 M KCl. The washed mycelia were resuspended in a 125 ml flask with 20 ml of protoplasting solution composed of 5 mg of GLUCANEX™ (Novozymes A/S) and 0.5 mg of chitinase (Sigma) per ml of 0.7 M KCl (filter sterilized) and incubated at 34° C., for 30 minutes with mixing at 80 rpm. The protoplasting solution was poured through a sterile funnel lined with MIRACLOTH® and rinsed with 50 ml of STC composed of 1 M sorbitol-10 mM Tris-HCl pH 6.5-10 mM CaCl₂. The flow-through was collected in two 50 ml polypropylene tubes. The tubes were spun in the centrifuge at 1300×g for 10 minutes at room temperature. The supernatant was discarded and the protoplast pellet was resuspended in 20 ml of STC buffer. The protoplasts were washed by two rounds pellet resuspension in 20 ml of STC buffer and centrifugation at 1300×g for 10 minutes at room temperature. The final pellet was resuspended in 2 ml of STC buffer. The protoplasts were counted by removing a 10 µl sample and counting them in a haemocytometer (VWR). The volume was adjusted with STC buffer to obtain a protoplast concentration of 2×10^7 per ml.

The plasmid expression vectors pShTh147 (Example 2) was prepared for transformation by restriction digestion with Pme I for 4 hours at 37° C. The approximately 5.2 kb expression cassette was separated from the vector sequences by 0.8% agarose gel electrophoresis in TBE buffer, and purified using a QIAQUICK® Gel Extraction Kit according to manufacturer's instructions.

Four transformation reactions were prepared by adding 100 µl of protoplast preparation above into four 12 ml polypropylene tubes. To each tube was added two micrograms of the digested pShTh147 bt2 fragment to a 250 µl polyethylene glycol (PEG) solution (60% w/v polyethylene glycol (PEG), 10 mM Tris 6.5, 10 mM CaCl) followed by gentle mixing and incubation at 37° C. for 30 minutes. Each transformation reaction was diluted with 6 ml of STC buffer, followed by plating three separate aliquots onto COVE plates. Each plate was then incubated at 34° C. for 7-10 days. Forty of the resulting transformants (designated ShTh147 transformants) were transferred to individual COVE plates and incubated at 34° C. for 5 days. Spore stocks were prepared by collecting the spores in 0.1% TWEEN® 80. Cultures were stored by preparing a glycerol stock of each (800 µl spore stock, 200 µl 0.1% TWEEN® 80) and frozen at -80° C.

Example 10

Production of Malic Acid in Shake Flask Cultures of *Aspergillus oryzae* Transformants Containing Expression Vector Fragments of pAMFs69, pRyan1, pSaMf21, pSaMf36, and pShTh147 (ShTh147)

Spores from ShTh147 transformants described in Example 9 and *Aspergillus oryzae* NRRL 3488 as a control were plated onto individual PDA plates and allowed to sporulate at 34° C. for 5 to 7 days. Spores were collected in 0.1% TWEEN® 80 and counted using a hemacytometer. Seed cultures were prepared in 250 mL flasks containing 100 mL of seed medium B and inoculated with 1 mL of harvested spores. Seed cultures were grown for approximately 22 hours at 30° C. with shaking at 200 rpm. Acid production cultures were prepared in 250 mL un baffled flasks containing 50 mL of acid production medium C and 3 mL of the 22 hour seed cultures. Cultures were incubated at 30° C. with shaking at 200 rpm for 3 days.

Quantitation of malic acid for the shake flask culture transformants was performed by Reverse Phase High Pressure Liquid Chromatography (RP-HPLC) using an 1200 Series Binary LC System and 1200 Series Diode Array Detector (DAD) (Agilent Technologies, Santa Clara, Calif. USA). Reverse phase separation was performed using an Aqua 5µ C18 125 Å 205×4.6 mm ID column and AQ C18 4×3.0 mm Security Guard Cartridge (Phenomenex, Inc., Torrance, Calif., USA). The mobile phase consisted of 10% methanol (HPLC grade) and 90% 145 mM phosphate pH 1.5 buffer.

Whole culture samples were removed and diluted 1:20 in HPLC Running Buffer composed of 900 ml of 145 mM phosphate buffer and 100 ml of methanol pH 1.50. The samples were then filtered through a 96 well 0.45 micron Durapore PVDF membrane into a 96 well plate for acid analysis.

RP-HPLC was performed using an injection volume of 10 µl at a flow rate of 0.7 ml/minute (isocratic) and column temperature at 20° C. Detection was at 210 nm, 4 nm bandwidth, with the reference at 360 nm, 40 nm bandwidth. The run time was 13 minutes. The void time was determined to be 3.8 minutes. The quantitative capabilities of the reverse phase method were determined for malic acid by performing replicate injections of serially diluted malic acid standards with concentrations ranging from 49.2-3.93 mM. The relative standard deviation for (RSD) for replicate injections was ≤5%. Malic acid shows $R^2 \geq 0.9999$.

After shake flask testing, six *Aspergillus oryzae* ShTh147 transformants were identified that produced malic acid at levels above the M727 control, including two that were improved 1.15× and 1.14×.

The present invention may be further described by the following numbered paragraphs:

- [1] A recombinant host cell comprising a heterologous polynucleotide that encodes a bicarbonate transporter, wherein the host cell is capable of producing a greater amount of a C4-dicarboxylic acid compared to the host cell without the heterologous polynucleotide when cultivated under the same conditions.
- [2] The recombinant host cell of paragraph [1], wherein the bicarbonate transporter is a sulfate-bicarbonate transporter.
- [3] The recombinant host cell of paragraph [1] or [2], wherein the bicarbonate transporter is selected from:
 - (a) a polypeptide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least

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91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof;

(b) a polypeptide encoded by a polynucleotide that hybridizes under low stringency conditions, medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii);

(c) a polypeptide encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v);

(d) a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof; and

(e) a fragment of (a), (b), (c), or (d) that has bicarbonate transporter activity.

[4] The recombinant host cell of any one of paragraphs [1]-[3], wherein the bicarbonate transporter has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof.

[5] The recombinant host cell of any one of paragraphs [1]-[4], wherein the bicarbonate transporter is encoded by a polynucleotide that hybridizes under low stringency conditions, medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (ii) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (iii) the full-length complementary strand of (i) or (ii).

[6] The recombinant host cell of any one of paragraphs [1]-[5], wherein the bicarbonate transporter is encoded by a polynucleotide having at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to (iv) SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof, (v) the cDNA sequence of SEQ ID NO: 1 or 3, or the mature polypeptide coding sequence thereof; or (vi) the full-length complementary strand of (iv) or (v).

[7] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof.

[8] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of SEQ ID NO: 2 or 4.

[9] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of SEQ ID NO: 2.

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[10] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of SEQ ID NO: 4.

[11] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 2 or 4.

[12] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 2.

[13] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter comprises or consists of the mature polypeptide sequence of SEQ ID NO: 4.

[14] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4, or the mature polypeptide sequence thereof.

[15] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2 or 4.

[16] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 2.

[17] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of SEQ ID NO: 4.

[18] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 2 or 4.

[19] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 2.

[20] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a variant comprising a substitution, deletion, and/or insertion of one or more (several) amino acids of the mature polypeptide sequence of SEQ ID NO: 4.

[21] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a fragment of SEQ ID NO: 2 or 4, wherein the fragment has bicarbonate transporter activity.

[22] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a fragment of SEQ ID NO: 2, wherein the fragment has bicarbonate transporter activity.

[23] The recombinant host cell of any one of paragraphs [1]-[6], wherein the bicarbonate transporter is a fragment of SEQ ID NO: 4, wherein the fragment has bicarbonate transporter activity.

[24] The recombinant host cell of any one of paragraphs [1]-[23], wherein the heterologous polynucleotide is operably linked to a promoter foreign to the polynucleotide.

[25] The recombinant host cell of any one of paragraphs [1]-[24], further comprising a heterologous second polynucleotide encoding a C4-dicarboxylic acid transporter

- (e.g., a heterologous polynucleotide encoding SEQ ID NO: 6, 27, 29, 32, 34, 36, 39, 41, or 43, or any related aspect thereof).
- [26] The recombinant host cell of paragraph [25], wherein the heterologous second polynucleotide is operably linked to a promoter foreign to the polynucleotide.
- [27] The recombinant host cell of any one of paragraphs [1]-[26], further comprising a heterologous third polynucleotide encoding a malate dehydrogenase (e.g., a heterologous polynucleotide encoding SEQ ID NO: 8 or 45, or any related aspect thereof).
- [28] The recombinant host cell of paragraph [27], wherein the heterologous third polynucleotide is operably linked to a promoter foreign to the polynucleotide.
- [29] The recombinant host cell of any one of paragraphs [1]-[28], further comprising a heterologous fourth polynucleotide encoding a pyruvate carboxylase (e.g., a heterologous polynucleotide encoding SEQ ID NO: 10, or any related aspect thereof).
- [30] The recombinant host cell of paragraphs [29], wherein the heterologous fourth polynucleotide is operably linked to a promoter foreign to the polynucleotide.
- [31] The recombinant host cell of any one of paragraphs [1]-[24], further comprising a heterologous second polynucleotide encoding a C4-dicarboxylic acid transporter, a heterologous third polynucleotide encoding a malate dehydrogenase, and a heterologous fourth polynucleotide encoding a pyruvate carboxylase.
- [32] The recombinant host cell of any one of paragraphs [1]-[31], wherein the host cell is a eukaryotic host cell.
- [33] The recombinant host cell of paragraph [32], wherein the host cell is a filamentous fungal host cell.
- [34] The recombinant host cell of paragraph [33], wherein the host cell is selected from the group consisting of an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Cryptococcus*, *Filobasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phlebia*, *Piromyces*, *Pleurotus*, *Rhizopus*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trametes*, and *Trichoderma*.
- [35] The recombinant host cell of paragraph [34], wherein the host cell is an *Aspergillus* host cell.
- [36] The recombinant host cell of paragraph [35], wherein the host cell is an *Aspergillus oryzae* host cell.
- [37] The recombinant host cell of paragraph [35], wherein the host cell is an *Aspergillus niger* host cell.
- [38] The recombinant host cell of any one of paragraphs [1]-[37], wherein the C4-dicarboxylic acid is selected from malic acid, succinic acid, oxaloacetic acid, malonic acid, and fumaric acid.
- [39] The recombinant host cell of paragraph [38], wherein the C4-dicarboxylic acid is malic acid.
- [40] The recombinant host cell of any one of paragraphs [1]-[39], wherein the cell is capable of C4-dicarboxylic acid volumetric productivity greater than about 0.1 g/L per hour, e.g., greater than about 0.2 g/L per hour, 0.5 g/L per hour, 0.6 g/L per hour, 0.7 g/L per hour, 0.8 g/L per hour, 0.9 g/L per hour, 1.0 g/L per hour, 1.1 g/L per hour, 1.2 g/L per hour, 1.3 g/L per hour, 1.5 g/L per hour, 1.75 g/L per hour, 2.0 g/L per hour, 2.25 g/L per hour, 2.5 g/L per hour, or 3.0 g/L per hour; or between about 0.1 g/L per hour and about 2.0 g/L per hour, e.g., between about 0.3 g/L per hour and about 1.7 g/L per hour, about 0.5 g/L per hour and about 1.5 g/L per hour, about 0.7 g/L per hour

- and about 1.3 g/L per hour, about 0.8 g/L per hour and about 1.2 g/L per hour, or about 0.9 g/L per hour and about 1.1 g/L per hour.
- [41] The recombinant host cell of any one of paragraphs [1]-[40], wherein the host cell is capable of producing a greater amount of the C4-dicarboxylic acid by at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 50%, or at least 100% compared to the host cell without the heterologous polynucleotide that encodes the bicarbonate transporter, when cultivated under the same conditions.
- [42] A composition comprising the recombinant host cell of any one of paragraphs [1]-[41].
- [43] The composition of paragraph [42], wherein the medium is a fermentable medium.
- [44] The composition of paragraph [42] or [43], further comprising a C4-dicarboxylic acid.
- [45] The composition of paragraph [44], wherein the C4-dicarboxylic acid is selected from malic acid, succinic acid, oxaloacetic acid, malonic acid, and fumaric acid.
- [46] The composition of paragraph [45], wherein the C4-dicarboxylic acid is malic acid.
- [47] The composition of any one of paragraphs [42]-[46], wherein the C4-dicarboxylic acid is at a titer greater than about 10 g/L, e.g., greater than about 25 g/L, 50 g/L, 75 g/L, 100 g/L, 125 g/L, 150 g/L, 160 g/L, 170 g/L, 180 g/L, 190 g/L, 200 g/L, 210 g/L, 225 g/L, 250 g/L, 275 g/L, 300 g/L, 325 g/L, 350 g/L, 400 g/L, or 500 g/L; or between about 10 g/L and about 500 g/L, e.g., between about 50 g/L and about 350 g/L, about 100 g/L and about 300 g/L, about 150 g/L and about 250 g/L, about 175 g/L and about 225 g/L, or about 190 g/L and about 210 g/L.
- [48] A method of producing a C4-dicarboxylic acid, comprising:
- (a) cultivating the recombinant host cell of any one of paragraphs [1]-[41] in a medium under suitable conditions to produce the C4-dicarboxylic acid; and
 - (b) recovering the C4-dicarboxylic acid.
- [49] The method of paragraph [48], wherein the medium is a fermentable medium.
- [50] The method of paragraph [48] or [49], wherein the C4-dicarboxylic acid is at a titer greater than about 10 g/L, e.g., greater than about 25 g/L, 50 g/L, 75 g/L, 100 g/L, 125 g/L, 150 g/L, 160 g/L, 170 g/L, 180 g/L, 190 g/L, 200 g/L, 210 g/L, 225 g/L, 250 g/L, 275 g/L, 300 g/L, 325 g/L, 350 g/L, 400 g/L, or 500 g/L; or between about 10 g/L and about 500 g/L, e.g., between about 50 g/L and about 350 g/L, about 100 g/L and about 300 g/L, about 150 g/L and about 250 g/L, about 175 g/L and about 225 g/L, or about 190 g/L and about 210 g/L.
- [51] The method of any one of paragraphs [48]-[50], wherein the amount of the produced C4-dicarboxylic acid is at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 30%, at least 50%, or at least 100% greater compared to cultivating the host cell without the polynucleotide encoding that encodes the bicarbonate transporter under the same conditions.
- [52] The method of any one of paragraphs [48]-[51], wherein the C4-dicarboxylic acid is selected from malic acid, succinic acid, oxaloacetic acid, malonic acid, and fumaric acid.
- [53] The method of paragraph [52], wherein the C4-dicarboxylic acid is malic acid.
- The invention described and claimed herein is not to be limited in scope by the specific aspects herein disclosed, since these aspects are intended as illustrations of several

aspects of the invention. Any equivalent aspects are intended to be within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled

in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. In the case of conflict, the present disclosure including definitions will control.

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Leu Tyr Ser Phe Val Ile Asn Pro Phe Ile Tyr Ala Ile Phe Gly Ser
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Ser Pro Leu Leu Ile Val Gly Pro Glu Ala Ala Gly Ser Leu Leu Thr
225    230    235    240
Gly Thr Ile Val Lys Thr Ser Val Arg Pro Gly Pro Ser Gly Glu Asp
245    250    255
Asp Glu Val Ala Asn Ala Ile Val Val Gly Ile Ala Thr Ala Met Ala
260    265    270

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Gly 275	Ala 280	Met 285	Ile 290	Leu 295	Ile 300	Ala 305	Gly 310	Leu 315	Thr 320	Arg 325	Leu 330	Gly 335	Phe 340	Leu 345	Asp 350
Asn 290	Val 295	Leu 300	Ser 305	Arg 310	Pro 315	Phe 320	Leu 325	Arg 330	Gly 335	Phe 340	Ile 345	Thr 350	Ala 355	Ile 360	Gly 365
Phe 305	Val 310	Ile 315	Phe 320	Val 325	Asp 330	Gln 335	Leu 340	Ile 345	Pro 350	Glu 355	Val 360	Gly 365	Leu 370	Thr 375	Glu 380
Leu 310	Ala 315	Lys 320	Glu 325	Ala 330	Gly 335	Val 340	Thr 345	His 350	Gly 355	Thr 360	Thr 365	Val 370	Asp 375	Lys 380	Leu 385
Met 315	Phe 320	Leu 325	Ile 330	Arg 335	Asn 340	Ile 345	Gly 350	Gly 355	Cys 360	His 365	Ala 370	Leu 375	Thr 380	Thr 385	Ala 390
Val 320	Ala 325	Phe 330	Gly 335	Ser 340	Phe 345	Ala 350	Ile 355	Ile 360	Met 365	Val 370	Phe 375	Arg 380	Thr 385	Leu 390	Lys 395
Lys 325	Met 330	Leu 335	Gln 340	Pro 345	Arg 350	Tyr 355	Pro 360	Gln 365	Val 370	Ile 375	Tyr 380	Leu 385	Pro 390	Asp 395	Arg 400
Ile 330	Leu 335	Val 340	Val 345	Ile 350	Leu 355	Ser 360	Ala 365	Val 370	Leu 375	Thr 380	Trp 385	His 390	Leu 395	Gly 400	Trp 405
Asp 335	Asp 340	Lys 345	Gly 350	Leu 355	Glu 360	Ile 365	Leu 370	Gly 375	Pro 380	Leu 385	Lys 390	Gln 395	Asn 400	Ala 405	Asn 410
Gly 340	Leu 345	Phe 350	Ala 355	Phe 360	Lys 365	Trp 370	Pro 375	Phe 380	Gln 385	Phe 390	Ser 395	Gln 400	Met 405	Lys 410	His 415
Val 345	Arg 350	Ala 355	Ala 360	Met 365	Ser 370	Thr 375	Ser 380	Phe 385	Val 390	Ile 395	Ala 400	Leu 405	Leu 410	Gly 415	Phe 420
Phe 350	Glu 355	Ser 360	Ser 365	Val 370	Ala 375	Ala 380	Lys 385	Gly 390	Leu 395	Ser 400	Gly 405	Glu 410	Ala 415	Arg 420	Gln 425
Glu 355	Gly 360	Val 365	Gln 370	Gly 375	Met 380	Pro 385	Val 390	Ser 395	Ala 400	Asn 405	Arg 410	Glu 415	Met 420	Val 425	Ala 430
Leu 360	Gly 365	Leu 370	Ala 375	Asn 380	Thr 385	Val 390	Gly 395	Gly 400	Cys 405	Phe 410	Met 415	Ala 420	Leu 425	Pro 430	Ala 435
Phe 365	Gly 370	Gly 375	Tyr 380	Ala 385	Arg 390	Ser 395	Lys 400	Val 405	Asn 410	Ala 415	Ser 420	Thr 425	Gly 430	Ala 435	Arg 440
Ser 370	Pro 375	Met 380	Ser 385	Ser 390	Ile 395	Phe 400	Leu 405	Ser 410	Ile 415	Ile 420	Thr 425	Phe 430	Val 435	Cys 440	Ile 445
Met 375	Val 380	Leu 385	Leu 390	Pro 395	Tyr 400	Leu 405	Tyr 410	Tyr 415	Leu 420	Pro 425	Lys 430	Ala 435	Val 440	Leu 445	Ser 450
Ser 380	Met 385	Ile 390	Ser 395	Val 400	Val 405	Ala 410	Phe 415	Ser 420	Leu 425	Ile 430	Glu 435	Glu 440	Cys 445	Pro 450	His 455
Asp 385	Val 390	Ala 395	Phe 400	Phe 405	Ile 410	Arg 415	Leu 420	Arg 425	Gly 430	Trp 435	Thr 440	Glu 445	Leu 450	Ala 455	Leu 460
Met 390	Leu 395	Leu 400	Ile 405	Phe 410	Val 415	Ser 420	Thr 425	Ile 430	Phe 435	Tyr 440	Ser 445	Leu 450	Glu 455	Leu 460	Gly 465
Ile 395	Ala 400	Leu 405	Gly 410	Ile 415	Gly 420	Leu 425	Ser 430	Ile 435	Leu 440	Ile 445	Leu 450	Ile 455	Arg 460	His 465	Ser 470
Thr 400	Gln 405	Pro 410	Arg 415	Ile 420	Gln 425	Ile 430	Leu 435	Gly 440	Lys 445	Ile 450	Ala 455	Gly 460	Thr 465	Thr 470	Asp 475
Arg 405	Phe 410	Asp 415	Asn 420	Ala 425	Glu 430	Leu 435	His 440	Pro 445	Glu 450	Ser 455	Val 460	Glu 465	Leu 470	Ile 475	Glu 480
Gly 410	Ala 415	Leu 420	Ile 425	Val 430	Lys 435	Ile 440	Pro 445	Glu 450	Pro 455	Leu 460	Thr 465	Phe 470	Ala 475	Asn 480	Thr 485
Gly 415	Glu 420	Leu 425	Lys 430	Asn 4											

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Asn Ile Ile Phe Asp Val His Gly Val Thr Ser Ile Asp Gly Ser Gly
 690 695 700
 Thr Gln Val Leu Tyr Glu Ile Val Asp Gly Tyr Ala Asp Gln Gly Val
 705 710 715 720
 Ser Val Phe Phe Cys Arg Val Ala Thr Arg Asn Val Phe Arg Met Phe
 725 730 735
 Glu Arg Ser Gly Ile Val Glu Arg Cys Gly Gly Ile Thr His Phe Val
 740 745 750
 His Gly Val Asp Glu Ala Leu Arg Leu Ala Glu Ser Glu Asp Glu Ile
 755 760 765
 Glu Ile
 770

<210> SEQ ID NO 3
 <211> LENGTH: 2657
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 3

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ttctccgtcg	gaacgatcga	cacatactcc	tatctcgagc	ccgaaccac	tcccgtgaa	180
tggctgaagg	aagtctgccc	tagctggcat	caggtgggcc	gttattttta	caaccttttc	240
cctttctct	cgtggattac	gaggtacaac	ttgcaatggt	tgtctggaga	tatgattgcc	300
ggtaagagcc	tttccactgt	gtttgatattg	atcgacaagt	agacaacata	ctcattggaa	360
tgcaggcgctc	acggtcggtg	ctgtggtcgt	tccgcaggga	atggcctacg	ctaaactggc	420
aaacctacct	gtagagtatg	gtctctatct	ctcgttcatg	ggtgttctca	tttattgggt	480
ttttgccacc	tcaaaggata	tcaccattgg	tgtaagtcac	tctgcaccca	tgtcagcatg	540
tatcttgcta	atatagtatc	ttccctgttc	agccggtggc	tgtcatgtct	acccttacag	600
gtaagatagt	tgccgaggcg	caaacgaagc	tcccagatgt	cgaagggcac	gtaatcgctt	660
cctgtttggc	tatcatttgt	ggagccgtgg	tttgcgctat	gggcctgctt	cggtgggat	720
ttatcggtga	tttcatctct	ctgccggcaa	tttcagcttt	catgacgggt	tccgccatca	780
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ccgccatggg	tgctagtgct	ttagctatgc	tgtaacattat	ccgttcgggt	tgcaattatg	960
gcgcgaagaa	gttcccccg	catgccaaag	tttggttctt	cgtttcgact	ttgcgcacag	1020
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acccgcggtt	caagctcctg	ggtaaagtcc	ctcgtgggtt	ccaacatgcg	gctgtccctc	1140
aggtaaatcc	gaggatcatc	agcgcatttg	ctagcgaact	tcctgcttcg	attattgtcc	1200
tgcttatcga	acacatcgct	atctcgaaat	cctttggccg	tgtaacaac	tacacaattg	1260
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gttaccacgc	gactggatcg	ttctcccgaa	ctgcaatcaa	atcgaaagcg	ggtgtccgca	1380
ccccacttgc	cgggtgttatt	actgcggttg	ttgtcctcct	cgcattttac	gctctgcccg	1440
ctgtcttctt	ttacatcccg	aaagcttccc	ttgtgggtgt	catcattcat	gcagtcgggtg	1500
acctcattac	cccaccaaac	accgtttacc	agttctggcg	cgtgtccctc	ctggatgcga	1560
tcattttctt	tatcggtggt	atcgtgactg	tcttcaccac	gattgagatc	ggcattttact	1620

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gtaccgtttg tgtgtctgtt gccattctgc tgttcgcgt cgccaaggcc cgcggtaaat 1680
tcttaggaag agtcactatc cactcgggtga tcggtgacca tctggtacag gatgatggga 1740
aatatgggtc tgccaactcc cctaattgtg ccagcgatga caaagatgaa ttgagccggt 1800
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cttatcctgg tatcttcac taccgattct cggaaggatt caactacccc aatgccaatc 1920
actacaccga ttatttggtc cagactatct tcaagcatat acgtgcgaca aatccgttct 1980
cctacggtaa accgggtgat cggccatgga ataactctgg ccctcgcagg ggcaagtctg 2040
aagatgacga gtcgcatttg cccttactgc aggtgtcat tcttgacttc tcatccgtca 2100
acaatgttga tgtgacctcg gtcagaacc tcatcgatgt ccgcaatcaa ctgcacctct 2160
acgcttcgcc taagactgtg cagtggcact ttgctcatat taacaaccgc tggacgaaac 2220
gagcccttgc agcagcaggt ttgggttcc catctccgga ctcgatgaa ggattccaga 2280
gatggaagcc aattttcagc gtggctgaga tcgaaggcag tgccctcgcc gcagctcatg 2340
cagagatggt gaacaacaga cacaccagc ataacatcaa gagcgaagac ctgcagcatg 2400
gcctcaagca cgattcagag accaccgagc gtgagacaca cggcatcgaa gaatcctccg 2460
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gcagtcgcgc aagggtcgct atgggtgcagg gcctcaaccg gccattcttc cacatcgacc 2580
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atgtccttga tgcatag 2657

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<210> SEQ ID NO 4
<211> LENGTH: 843
<212> TYPE: PRT
<213> ORGANISM: Aspergillus oryzae

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<400> SEQUENCE: 4

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Met Pro Gly Asp Leu Lys Thr Lys Ile Gly His Gly Ala Ala Lys Ala
1           5           10          15

Leu Gly Ile Lys Ile Pro Tyr Arg Asp Pro Leu Gly Val His Ala Asp
20          25          30

Pro Val Thr Arg Gly Glu Ser Met Phe Ser Val Gly Thr Ile Asp Thr
35          40          45

Tyr Ser Tyr Leu Glu Pro Glu Pro Thr Pro Ala Glu Trp Leu Lys Glu
50          55          60

Val Cys Pro Ser Trp His Gln Val Gly Arg Tyr Phe Tyr Asn Leu Phe
65          70          75          80

Pro Phe Leu Ser Trp Ile Thr Arg Tyr Asn Leu Gln Trp Leu Leu Gly
85          90          95

Asp Met Ile Ala Gly Val Thr Val Gly Ala Val Val Val Pro Gln Gly
100         105         110

Met Ala Tyr Ala Lys Leu Ala Asn Leu Pro Val Glu Tyr Gly Leu Tyr
115         120         125

Ser Ser Phe Met Gly Val Leu Ile Tyr Trp Phe Phe Ala Thr Ser Lys
130         135         140

Asp Ile Thr Ile Gly Pro Val Ala Val Met Ser Thr Leu Thr Gly Lys
145         150         155         160

Ile Val Ala Glu Ala Gln Thr Lys Leu Pro Asp Val Glu Gly His Val
165         170         175

Ile Ala Ser Cys Leu Ala Ile Ile Cys Gly Ala Val Val Cys Ala Met

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180							185					190				
Gly	Leu	Leu	Arg	Leu	Gly	Phe	Ile	Val	Asp	Phe	Ile	Pro	Leu	Pro	Ala	
		195					200					205				
Ile	Ser	Ala	Phe	Met	Thr	Gly	Ser	Ala	Ile	Asn	Ile	Cys	Ser	Gly	Gln	
	210					215					220					
Val	Lys	Asp	Met	Leu	Gly	Glu	Thr	Ala	Asp	Phe	Ser	Thr	Lys	Asp	Ser	
	225				230					235					240	
Thr	Tyr	Leu	Val	Ile	Ile	Asn	Thr	Leu	Lys	His	Leu	Pro	Ser	Ala	Lys	
			245						250					255		
Ile	Asp	Ala	Ala	Met	Gly	Val	Ser	Ala	Leu	Ala	Met	Leu	Tyr	Ile	Ile	
			260						265				270			
Arg	Ser	Gly	Cys	Asn	Tyr	Gly	Ala	Lys	Lys	Phe	Pro	Arg	His	Ala	Lys	
		275					280					285				
Val	Trp	Phe	Phe	Val	Ser	Thr	Leu	Arg	Thr	Val	Phe	Val	Ile	Leu	Phe	
	290					295					300					
Tyr	Thr	Met	Ile	Ser	Ala	Ala	Val	Asn	Leu	His	Arg	Arg	Ser	Asn	Pro	
	305				310					315					320	
Arg	Phe	Lys	Leu	Leu	Gly	Lys	Val	Pro	Arg	Gly	Phe	Gln	His	Ala	Ala	
			325						330					335		
Val	Pro	Gln	Val	Asn	Ser	Arg	Ile	Ile	Ser	Ala	Phe	Ala	Ser	Glu	Leu	
			340					345					350			
Pro	Ala	Ser	Ile	Ile	Val	Leu	Leu	Ile	Glu	His	Ile	Ala	Ile	Ser	Lys	
		355					360					365				
Ser	Phe	Gly	Arg	Val	Asn	Asn	Tyr	Thr	Ile	Asp	Pro	Ser	Gln	Glu	Leu	
	370					375					380					
Val	Ala	Ile	Gly	Val	Ser	Asn	Leu	Leu	Gly	Pro	Phe	Leu	Gly	Gly	Tyr	
	385				390					395					400	
Pro	Ala	Thr	Gly	Ser	Phe	Ser	Arg	Thr	Ala	Ile	Lys	Ser	Lys	Ala	Gly	
			405						410					415		
Val	Arg	Thr	Pro	Leu	Ala	Gly	Val	Ile	Thr	Ala	Val	Val	Val	Leu	Leu	
			420					425					430			
Ala	Ile	Tyr	Ala	Leu	Pro	Ala	Val	Phe	Phe	Tyr	Ile	Pro	Lys	Ala	Ser	
		435					440					445				
Leu	Ala	Gly	Val	Ile	Ile	His	Ala	Val	Gly	Asp	Leu	Ile	Thr	Pro	Pro	
	450					455					460					
Asn	Thr	Val	Tyr	Gln	Phe	Trp	Arg	Val	Ser	Pro	Leu	Asp	Ala	Ile	Ile	
	465				470					475					480	
Phe	Phe	Ile	Gly	Val	Ile	Val	Thr	Val	Phe	Thr	Thr	Ile	Glu	Ile	Gly	
			485						490					495		
Ile	Tyr	Cys	Thr	Val	Cys	Val	Ser	Val	Ala	Ile	Leu	Leu	Phe	Arg	Val	
			500					505					510			
Ala	Lys	Ala	Arg	Gly	Gln	Phe	Leu	Gly	Arg	Val	Thr	Ile	His	Ser	Val	
		515					520					525				
Ile	Gly	Asp	His	Leu	Val	Gln	Asp	Asp	Gly	Lys	Tyr	Gly	Ser	Ala	Asn	
	530					535					540					
Ser	Pro	Asn	Ala	Ala	Ser	Asp	Asp	Lys	Asp	Glu	Leu	Ser	Arg	Ser	Ile	
	545				550					555					560	
Phe	Leu	Pro	Ile	Asn	His	Thr	Asp	Gly	Ser	Asn	Pro	Asp	Val	Glu	Val	
			565					570						575		
Gln	Gln	Pro	Tyr	Pro	Gly	Ile	Phe	Ile	Tyr	Arg	Phe	Ser	Glu	Gly	Phe	
			580					585					590			
Asn	Tyr	Pro	Asn	Ala	Asn	His	Tyr	Thr	Asp	Tyr	Leu	Val	Gln	Thr	Ile	
		595					600						605			

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Phe Lys His Thr Arg Arg Thr Asn Pro Phe Ser Tyr Gly Lys Pro Gly
 610 615 620
 Asp Arg Pro Trp Asn Asn Pro Gly Pro Arg Arg Gly Lys Ser Glu Asp
 625 630 635 640
 Asp Glu Ser His Leu Pro Leu Leu Gln Ala Val Ile Leu Asp Phe Ser
 645 650 655
 Ser Val Asn Asn Val Asp Val Thr Ser Val Gln Asn Leu Ile Asp Val
 660 665 670
 Arg Asn Gln Leu Asp Leu Tyr Ala Ser Pro Lys Thr Val Gln Trp His
 675 680 685
 Phe Ala His Ile Asn Asn Arg Trp Thr Lys Arg Ala Leu Ala Ala Ala
 690 695 700
 Gly Phe Gly Phe Pro Ser Pro Asp Ser Asp Glu Gly Phe Gln Arg Trp
 705 710 715 720
 Lys Pro Ile Phe Ser Val Ala Glu Ile Glu Gly Ser Ala Ser Ala Ala
 725 730 735
 Ala His Ala Glu Met Val Asn Asn Arg His Thr Gln His Asn Ile Lys
 740 745 750
 Ser Glu Asp Leu Glu His Gly Leu Lys His Asp Ser Glu Thr Thr Glu
 755 760 765
 Arg Glu Thr His Gly Ile Glu Glu Ser Ser Asp Ala Ser Ser Thr Arg
 770 775 780
 Glu Asp Lys Leu Gln Arg Asp Leu Lys Asp Ser Lys Ala Tyr Arg Ser
 785 790 795 800
 Arg Arg Arg Val Ala Met Val Gln Gly Leu Asn Arg Pro Phe Phe His
 805 810 815
 Ile Asp Leu Thr Ser Ala Leu Gln Ser Ala Leu Ala Asn Ala Gly Glu
 820 825 830
 Gln Pro Asp Pro Lys Met Asn Val Leu Asp Ala
 835 840

<210> SEQ ID NO 5

<211> LENGTH: 1257

<212> TYPE: DNA

<213> ORGANISM: *Aspergillus aculeatus*

<400> SEQUENCE: 5

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gcctgcgaga agtccgtcaa ccccgagacc aaagtctccc agcctcagga atctccatt	120
atcagcaata atgaacatca ggagtttggt aagctgggca tccgccaaac gctgcgtcat	180
ttcacctggg cctggtatac cctaaccatg agcgcaggtg gactggccct tcttctcgc	240
aaccagccgt atcaattcaa ggggttgaag gagataggcc tgggtgtata catagccaat	300
ctcgtcttct ttactatcat cggtctcttt atgatcacca gggttgttct ttacaacaac	360
ctgatggact ctctccgcca cgaccgagaa gggttcttct ttccaacctt ctggctctcc	420
atcgccacca tgattagtgg tctatctgcc tacttctcta ctgaagacac gcaccgctc	480
aattatgctc tcgagggtct cttctgggct tactgtatct tcacgtttgc ctcagcagt	540
atccagtact cctttgtctt ctctatcac acgttccttc tgcaaaactat gatgccatca	600
tggatcttac cggcattccc tatcatgtg agcggaacca ttgcctctgc cgttccagc	660
taccagcctg cgggtgtctg cagcctatg attgttgccg gcatcacgtt ccagggactc	720
ggattctgca tcagcttcat gatgtacgcc cactacatcg ggcgtctgat ggagacgggc	780

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atcccttcga gcgagcaacg tctgggtatg ttcattctgtg tcggccccc tgccttcacg      840
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ggtggcatgg acgaccgtca catcatgcga gtactggccg tctgcgcggg catgttctctc     960
tgggctctga gcatttggtt cttctgtgtc gctctgggct cagttgtgcg ggcgcctccc    1020
catgatttcc acctcaactg gtgggctatg gtcttcctta acaccggact cactctcgcc    1080
accatcacc cggccaagtc actggacagt gccgcgttga aatgggtggg cgtgggcatg     1140
tccctctgcg tgatctgcat gttcatcttc gtcttcgtga gcaccattag ggctgttctc    1200
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<210> SEQ ID NO 6

<211> LENGTH: 418

<212> TYPE: PRT

<213> ORGANISM: Aspergillus aculeatus

<400> SEQUENCE: 6

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Thr Leu Asn His Ala Cys Glu Lys Ser Val Asn Pro Glu Ala Lys Val
20            25            30
Ser Gln Pro Gln Glu Ser Pro Ile Ile Ser Asn Asn Glu His Gln Glu
35            40            45
Phe Val Lys Leu Gly Ile Arg Gln Arg Leu Arg His Phe Thr Trp Ala
50            55            60
Trp Tyr Thr Leu Thr Met Ser Ala Gly Gly Leu Ala Leu Leu Leu Arg
65            70            75            80
Asn Gln Pro Tyr Gln Phe Lys Gly Leu Lys Glu Ile Gly Leu Val Val
85            90            95
Tyr Ile Ala Asn Leu Val Phe Phe Thr Ile Ile Gly Ser Leu Met Ile
100           105           110
Thr Arg Phe Val Leu Tyr Asn Asn Leu Met Asp Ser Leu Arg His Asp
115           120           125
Arg Glu Gly Phe Phe Phe Pro Thr Phe Trp Leu Ser Ile Ala Thr Met
130           135           140
Ile Ser Gly Leu Ser Ala Tyr Phe Ser Thr Glu Asp Thr His Arg Leu
145           150           155           160
Asn Tyr Ala Leu Glu Gly Leu Phe Trp Ala Tyr Cys Ile Phe Thr Phe
165           170           175
Ala Ser Ala Val Ile Gln Tyr Ser Phe Val Phe Ser Tyr His Thr Phe
180           185           190
Pro Leu Gln Thr Met Met Pro Ser Trp Ile Leu Pro Ala Phe Pro Ile
195           200           205
Met Leu Ser Gly Thr Ile Ala Ser Ala Ala Ser Ser Tyr Gln Pro Ala
210           215           220
Val Ser Ala Thr Pro Met Ile Val Ala Gly Ile Thr Phe Gln Gly Leu
225           230           235           240
Gly Phe Cys Ile Ser Phe Met Met Tyr Ala His Tyr Ile Gly Arg Leu
245           250           255
Met Glu Thr Gly Ile Pro Ser Ser Glu His Arg Pro Gly Met Phe Ile
260           265           270
Cys Val Gly Pro Pro Ala Phe Thr Leu Leu Ala Ile Ile Gly Met Ala
275           280           285

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Asn Gly Leu Pro Glu Gly Phe Ser Ile Leu Gly Asp Gly Gly Met Asp
 290 295 300
 Asp Arg His Ile Met Arg Val Leu Ala Val Cys Ala Gly Met Phe Leu
 305 310 315 320
 Trp Ala Leu Ser Ile Trp Phe Phe Cys Val Ala Leu Gly Ser Val Val
 325 330 335
 Arg Ala Pro Pro His Asp Phe His Leu Asn Trp Trp Ala Met Val Phe
 340 345 350
 Pro Asn Thr Gly Leu Thr Leu Ala Thr Ile Thr Leu Ala Lys Ser Leu
 355 360 365
 Asp Ser Ala Ala Leu Lys Trp Val Gly Val Gly Met Ser Leu Cys Val
 370 375 380
 Ile Cys Met Phe Ile Phe Val Phe Val Ser Thr Val Arg Ala Val Leu
 385 390 395 400
 Leu Lys Arg Ile Met Trp Pro Gly Arg Asp Glu Asp Val Ser Glu Leu
 405 410 415
 Phe Glu

<210> SEQ ID NO 7
 <211> LENGTH: 1430
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 7

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cttacaaccc tggtcacaat atgaccttgt tcgatactga ctatctccca agccactgtc	180
tctctgttg aagacctgtc ccttagttga agagcttgct ctctacgatg ttgtgaacac	240
ccctgggtgt gctgctgac tatcccatat ctcgtctatc gctgtacgtt actgccacaa	300
tgcaaatgc ccgatggaag aggcgaaaaa tggtagcttg cttacctggg cgattagaaa	360
atctctggtt ttctgccccaa agatgatggg ctgaagcagg cccttactgg tgctaataatt	420
gttgctatcc cggtcgggat tccccgtaag tccctaccct ttcgcattgc tcctcgtatg	480
ttcgctgggt gccagtttct tgatagttga taggcaagcc tggtagtacc cgtgacgacc	540
tcttcaagat caacgcgggc atagtgcgag acttggtcaa gggtagcgcc gagttctgcc	600
ccaaggcctt tgttctgggt atctcaaacc ccgttaattc tactgttctt attgctgcag	660
aggtgctcaa agccgctggc gtctttgacc cgaagcgctt ctttgggtgc accacactgg	720
acgtcgttgc tgcagagact ttcacccaag agttctcggg ccagaaggat ccttctgctg	780
ttcaaatacc agttgttggt ggccactctg gagagaccat tgtccccctc ttcagcaaga	840
ctacccccgc aattcagata cccgaggaga agtatgacgc actgatccac cgtaggttgt	900
cccaaagaat ctcatagaata tcttgctgta agcactaact atgcttcagg cgtccaattt	960
ggtaggagat aggtggtcca agctaaggac ggtgctggtt ccgccacctt gtctatggcc	1020
tatgccggtt acaggtaggg atgctgcgta ccgtgagagc actcgcgggt aacatgccat	1080
agggttcgct agagtgtaat caaagcttca aagggtcaaa cgggtattgt cgagcctacc	1140
ttcgtctacc tgcttgaat tcccgcggt gatgagatcg ttaaggcaac tggcgtggaa	1200
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tatcacgcca ggctaacgct attaaacaga ctaatggcgc agagaaggct agcaacgttc	1320
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gtaatatcga gaaaggcacg gacttcgtta agaaccacc accaaagtaa 1430

<210> SEQ ID NO 8
 <211> LENGTH: 330
 <212> TYPE: PRT
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 8

Met Val Lys Ala Ala Val Leu Gly Ala Ser Gly Gly Ile Gly Gln Pro
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 Leu Ser Leu Leu Leu Lys Thr Cys Pro Leu Val Glu Glu Leu Ala Leu
 20 25 30
 Tyr Asp Val Val Asn Thr Pro Gly Val Ala Ala Asp Leu Ser His Ile
 35 40 45
 Ser Ser Ile Ala Lys Ile Ser Gly Phe Leu Pro Lys Asp Asp Gly Leu
 50 55 60
 Lys Gln Ala Leu Thr Gly Ala Asn Ile Val Val Ile Pro Ala Gly Ile
 65 70 75 80
 Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Lys Ile Asn Ala
 85 90 95
 Gly Ile Val Arg Asp Leu Val Lys Gly Ile Ala Glu Phe Cys Pro Lys
 100 105 110
 Ala Phe Val Leu Val Ile Ser Asn Pro Val Asn Ser Thr Val Pro Ile
 115 120 125
 Ala Ala Glu Val Leu Lys Ala Ala Gly Val Phe Asp Pro Lys Arg Leu
 130 135 140
 Phe Gly Val Thr Thr Leu Asp Val Val Arg Ala Glu Thr Phe Thr Gln
 145 150 155 160
 Glu Phe Ser Gly Gln Lys Asp Pro Ser Ala Val Gln Ile Pro Val Val
 165 170 175
 Gly Gly His Ser Gly Glu Thr Ile Val Pro Leu Phe Ser Lys Thr Thr
 180 185 190
 Pro Ala Ile Gln Ile Pro Glu Glu Lys Tyr Asp Ala Leu Ile His Arg
 195 200 205
 Val Gln Phe Gly Gly Asp Glu Val Val Gln Ala Lys Asp Gly Ala Gly
 210 215 220
 Ser Ala Thr Leu Ser Met Ala Tyr Ala Gly Tyr Arg Phe Ala Glu Ser
 225 230 235 240
 Val Ile Lys Ala Ser Lys Gly Gln Thr Gly Ile Val Glu Pro Thr Phe
 245 250 255
 Val Tyr Leu Pro Gly Ile Pro Gly Gly Asp Glu Ile Val Lys Ala Thr
 260 265 270
 Gly Val Glu Phe Phe Ser Thr Leu Val Thr Leu Gly Thr Asn Gly Ala
 275 280 285
 Glu Lys Ala Ser Asn Val Leu Glu Gly Val Thr Glu Lys Glu Lys Lys
 290 295 300
 Leu Leu Glu Ala Cys Thr Lys Gly Leu Lys Gly Asn Ile Glu Lys Gly
 305 310 315 320
 Ile Asp Phe Val Lys Asn Pro Pro Pro Lys
 325 330

<210> SEQ ID NO 9
 <211> LENGTH: 3643
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

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<400> SEQUENCE: 9

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cacttcacaga	agatccctgt	cgccaaccgt	ggtgagatcc	ccattcgtat	cttcagaacg	180
gcccacgagc	tgtcattgca	gacggttgct	atctactctc	atgaggatcg	actgtcaatg	240
caccgtcaaa	aggccgatga	ggcctacatg	attggccacc	gcggtcagta	caccocctgtc	300
ggtgcgtacc	tggcgggcga	tgagatcacc	aagatcgccc	tggagcacgg	tgtccagctg	360
atccaccccg	gctacggttt	cttgtccgag	aacgcccact	tcgcccgcga	ggttgagaac	420
gccggcattg	tctttgtggg	accactccc	gataccattg	acagcttggg	tgacaagggtg	480
tcggcccgctc	ggctggccat	taagtgcgag	gtccctgtcg	ttccgggtac	ggaggggccc	540
gtcgcgcgt	atgaggaggt	caaggcgctc	acagacacct	atggcttccc	catcatcacc	600
aaggctgcct	ttggcgggtg	tggccgtggt	atgcgtgtgg	tcctgacca	ggccgagctg	660
cgtgactcgt	tcgagcgagc	cacctctgag	gcccgcctcg	ccttcggcaa	tggtaccgtc	720
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cagctcgagg	tcggtatcaa	ggctgttcat	gctgccgagg	gtgttgtcga	ggccaccatg	2160
tgctacagcg	gtgacatgct	gaacccccac	aagaagtaca	acctggagta	ctacatggcc	2220
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gtgctgaagc cccaggccgc tcgcctgttg gtgggtcca tccgtcagcg ctacctgac 2340
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tgtgcccagg cgggtgcca cgccgtggac gccgcgaccg acagcatgtc cggtatgacc 2460
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<210> SEQ ID NO 10

<211> LENGTH: 1193

<212> TYPE: PRT

<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 10

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Met Ala Ala Pro Phe Arg Gln Pro Glu Glu Ala Val Asp Asp Thr Glu
1           5           10          15

Phe Ile Asp Asp His His Glu His Leu Arg Asp Thr Val His His Arg
20        25        30

Leu Arg Ala Asn Ser Ser Ile Met His Phe Gln Lys Ile Leu Val Ala
35        40        45

Asn Arg Gly Glu Ile Pro Ile Arg Ile Phe Arg Thr Ala His Glu Leu
50        55        60

Ser Leu Gln Thr Val Ala Ile Tyr Ser His Glu Asp Arg Leu Ser Met
65        70        75        80

His Arg Gln Lys Ala Asp Glu Ala Tyr Met Ile Gly His Arg Gly Gln
85        90        95

Tyr Thr Pro Val Gly Ala Tyr Leu Ala Gly Asp Glu Ile Ile Lys Ile
100       105       110

Ala Leu Glu His Gly Val Gln Leu Ile His Pro Gly Tyr Gly Phe Leu
115       120       125

Ser Glu Asn Ala Asp Phe Ala Arg Lys Val Glu Asn Ala Gly Ile Val

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130	135	140
Phe Val Gly Pro Thr	Pro Asp Thr Ile Asp Ser	Leu Gly Asp Lys Val
145	150	155
Ser Ala Arg Arg Leu Ala Ile Lys Cys Glu Val	Pro Val Val Pro Gly	
	165	170
Thr Glu Gly Pro Val Glu Arg Tyr Glu Glu Val	Lys Ala Phe Thr Asp	
	180	185
Thr Tyr Gly Phe Pro Ile Ile Ile Lys Ala Ala Phe Gly Gly Gly Gly		
	195	200
Arg Gly Met Arg Val Val Arg Asp Gln Ala Glu Leu Arg Asp Ser Phe		
	210	215
Glu Arg Ala Thr Ser Glu Ala Arg Ser Ala Phe Gly Asn Gly Thr Val		
	225	230
Phe Val Glu Arg Phe Leu Asp Lys Pro Lys His Ile Glu Val Gln Leu		
	245	250
Leu Gly Asp Ser His Gly Asn Val Val His Leu Phe Glu Arg Asp Cys		
	260	265
Ser Val Gln Arg Arg His Gln Lys Val Val Glu Val Ala Pro Ala Lys		
	275	280
Asp Leu Pro Ala Asp Val Arg Asp Arg Ile Leu Ala Asp Ala Val Lys		
	290	295
Leu Ala Lys Ser Val Asn Tyr Arg Asn Ala Gly Thr Ala Glu Phe Leu		
	305	310
Val Asp Gln Gln Asn Arg His Tyr Phe Ile Glu Ile Asn Pro Arg Ile		
	325	330
Gln Val Glu His Thr Ile Thr Glu Glu Ile Thr Gly Ile Asp Ile Val		
	340	345
Ala Ala Gln Ile Gln Ile Ala Ala Gly Ala Ser Leu Glu Gln Leu Gly		
	355	360
Leu Thr Gln Asp Arg Ile Ser Ala Arg Gly Phe Ala Ile Gln Cys Arg		
	370	375
Ile Thr Thr Glu Asp Pro Ala Lys Gly Phe Ser Pro Asp Thr Gly Lys		
	385	390
Ile Glu Val Tyr Arg Ser Ala Gly Gly Asn Gly Val Arg Leu Asp Gly		
	405	410
Gly Asn Gly Phe Ala Gly Ala Ile Ile Thr Pro His Tyr Asp Ser Met		
	420	425
Leu Val Lys Cys Thr Cys Arg Gly Ser Thr Tyr Glu Ile Ala Arg Arg		
	435	440
Lys Val Val Arg Ala Leu Val Glu Phe Arg Ile Arg Gly Val Lys Thr		
	450	455
Asn Ile Pro Phe Leu Thr Ser Leu Leu Ser His Pro Thr Phe Val Asp		
	465	470
Gly Asn Cys Trp Thr Thr Phe Ile Asp Asp Thr Pro Glu Leu Phe Ser		
	485	490
Leu Val Gly Ser Gln Asn Arg Ala Gln Lys Leu Leu Ala Tyr Leu Gly		
	500	505
Asp Val Ala Val Asn Gly Ser Ser Ile Lys Gly Gln Ile Gly Glu Pro		
	515	520
Lys Leu Lys Gly Asp Val Ile Lys Pro Lys Leu Phe Asp Ala Glu Gly		
	530	535
Lys Pro Leu Asp Val Ser Ala Pro Cys Thr Lys Gly Trp Lys Gln Ile		
	545	550
		555
		560

Leu	Asp	Arg	Glu	Gly	Pro	Ala	Ala	Phe	Ala	Lys	Ala	Val	Arg	Ala	Asn	
				565					570					575		
Lys	Gly	Cys	Leu	Ile	Met	Asp	Thr	Thr	Trp	Arg	Asp	Ala	His	Gln	Ser	
				580					585					590		
Leu	Leu	Ala	Thr	Arg	Val	Arg	Thr	Ile	Asp	Leu	Leu	Asn	Ile	Ala	His	
				595					600					605		
Glu	Thr	Ser	Tyr	Ala	Tyr	Ser	Asn	Ala	Tyr	Ser	Leu	Glu	Cys	Trp	Gly	
				610					615					620		
Gly	Ala	Thr	Phe	Asp	Val	Ala	Met	Arg	Phe	Leu	Tyr	Glu	Asp	Pro	Trp	
				625					630					635		
Asp	Arg	Leu	Arg	Lys	Met	Arg	Lys	Ala	Val	Pro	Asn	Ile	Pro	Phe	Gln	
				645					650					655		
Met	Leu	Leu	Arg	Gly	Ala	Asn	Gly	Val	Ala	Tyr	Ser	Ser	Leu	Pro	Asp	
				660					665					670		
Asn	Ala	Ile	Tyr	His	Phe	Cys	Lys	Gln	Ala	Lys	Lys	Cys	Gly	Val	Asp	
				675					680					685		
Ile	Phe	Arg	Val	Phe	Asp	Ala	Leu	Asn	Asp	Val	Asp	Gln	Leu	Glu	Val	
				690					695					700		
Gly	Ile	Lys	Ala	Val	His	Ala	Ala	Glu	Gly	Val	Val	Glu	Ala	Thr	Met	
				705					710					715		
Cys	Tyr	Ser	Gly	Asp	Met	Leu	Asn	Pro	His	Lys	Lys	Tyr	Asn	Leu	Glu	
				725					730					735		
Tyr	Tyr	Met	Ala	Leu	Val	Asp	Lys	Ile	Val	Ala	Met	Lys	Pro	His	Ile	
				740					745					750		
Leu	Gly	Ile	Lys	Asp	Met	Ala	Gly	Val	Leu	Lys	Pro	Gln	Ala	Ala	Arg	
				755					760					765		
Leu	Leu	Val	Gly	Ser	Ile	Arg	Gln	Arg	Tyr	Pro	Asp	Leu	Pro	Ile	His	
				770					775					780		
Val	His	Thr	His	Asp	Ser	Ala	Gly	Thr	Gly	Val	Ala	Ser	Met	Ile	Ala	
				785					790					795		
Cys	Ala	Gln	Ala	Gly	Ala	Asp	Ala	Val	Asp	Ala	Ala	Thr	Asp	Ser	Met	
				805					810					815		
Ser	Gly	Met	Thr	Ser	Gln	Pro	Ser	Ile	Gly	Ala	Ile	Leu	Ala	Ser	Leu	
				820					825					830		
Glu	Gly	Thr	Glu	Gln	Asp	Pro	Gly	Leu	Asn	Leu	Ala	His	Val	Arg	Ala	
				835					840					845		
Ile	Asp	Ser	Tyr	Trp	Ala	Gln	Leu	Arg	Leu	Leu	Tyr	Ser	Pro	Phe	Glu	
				850					855					860		
Ala	Gly	Leu	Thr	Gly	Pro	Asp	Pro	Glu	Val	Tyr	Glu	His	Glu	Ile	Pro	
				865					870					875		
Gly	Gly	Gln	Leu	Thr	Asn	Leu	Ile	Phe	Gln	Ala	Ser	Gln	Leu	Gly	Leu	
				885					890					895		
Gly	Gln	Gln	Trp	Ala	Glu	Thr	Lys	Lys	Ala	Tyr	Glu	Ala	Ala	Asn	Asp	
				900					905					910		
Leu	Leu	Gly	Asp	Ile	Val	Lys	Val	Thr	Pro	Thr	Ser	Lys	Val	Val	Gly	
				915					920					925		
Asp	Leu	Ala	Gln	Phe	Met	Val	Ser	Asn	Lys	Leu	Thr	Pro	Glu	Asp	Val	
				930					935					940		
Val	Glu	Arg	Ala	Gly	Glu	Leu	Asp	Phe	Pro	Gly	Ser	Val	Leu	Glu	Phe	
				945					950					955		
Leu	Glu	Gly	Leu	Met	Gly	Gln	Pro	Phe								

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Arg Ser Arg Ala Leu Arg Asp Arg Arg Lys Leu Glu Lys Arg Pro Gly
 980 985 990

 Leu Tyr Leu Glu Pro Leu Asp Leu Ala Lys Ile Lys Ser Gln Ile Arg
 995 1000 1005

 Glu Lys Phe Gly Ala Ala Thr Glu Tyr Asp Val Ala Ser Tyr Ala
 1010 1015 1020

 Met Tyr Pro Lys Val Phe Glu Asp Tyr Lys Lys Phe Val Gln Lys
 1025 1030 1035

 Phe Gly Asp Leu Ser Val Leu Pro Thr Arg Tyr Phe Leu Ala Lys
 1040 1045 1050

 Pro Glu Ile Gly Glu Glu Phe His Val Glu Leu Glu Lys Gly Lys
 1055 1060 1065

 Val Leu Ile Leu Lys Leu Leu Ala Ile Gly Pro Leu Ser Glu Gln
 1070 1075 1080

 Thr Gly Gln Arg Glu Val Phe Tyr Glu Val Asn Gly Glu Val Arg
 1085 1090 1095

 Gln Val Ala Val Asp Asp Asn Lys Ala Ser Val Asp Asn Thr Ser
 1100 1105 1110

 Arg Pro Lys Ala Asp Val Gly Asp Ser Ser Gln Val Gly Ala Pro
 1115 1120 1125

 Met Ser Gly Val Val Val Glu Ile Arg Val His Asp Gly Leu Glu
 1130 1135 1140

 Val Lys Lys Gly Asp Pro Leu Ala Val Leu Ser Ala Met Lys Met
 1145 1150 1155

 Glu Met Val Ile Ser Ala Pro His Ser Gly Lys Val Ser Ser Leu
 1160 1165 1170

 Leu Val Lys Glu Gly Asp Ser Val Asp Gly Gln Asp Leu Val Cys
 1175 1180 1185

 Lys Ile Val Lys Ala
 1190

<210> SEQ ID NO 11
 <211> LENGTH: 40
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 11

gtgatagaac atcgctccata atggaatcca gcgctgtaca

40

<210> SEQ ID NO 12
 <211> LENGTH: 40
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 12

gtgtcagtc cctctagtta tcagatttca atctcgtctt

40

<210> SEQ ID NO 13
 <211> LENGTH: 20
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 13

gaacaggaag aaatccaaaa

20

<210> SEQ ID NO 14
 <211> LENGTH: 20
 <212> TYPE: DNA

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<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 14

gtcggcatag ccactgcaat                                20

<210> SEQ ID NO 15
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 15

tgttgccgcc aagggactta                                20

<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 16

ccgagagcgt tgagttaatc                                20

<210> SEQ ID NO 17
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 17

agcattaggg ctagctccgt                                20

<210> SEQ ID NO 18
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 18

ccaagatgcc atgtcaggac                                20

<210> SEQ ID NO 19
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 19

tcacaaaaga gtagaggcca                                20

<210> SEQ ID NO 20
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 20

tgtgatagaa catcgtccat aatgcacgac cacagc            36

<210> SEQ ID NO 21
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Aspergillus oryzae

<400> SEQUENCE: 21

gtgtcagtca cctctagtta tcattcgaac aactcggaca        40

<210> SEQ ID NO 22
<211> LENGTH: 36

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<212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*
 <400> SEQUENCE: 22
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<210> SEQ ID NO 23
 <211> LENGTH: 40
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*
 <400> SEQUENCE: 23
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<210> SEQ ID NO 24
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*
 <400> SEQUENCE: 24
 tagaacatcg tccataatgg cggctccgtt tcgtca 36

<210> SEQ ID NO 25
 <211> LENGTH: 40
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*
 <400> SEQUENCE: 25
 gtgtcagtc cctctagtta ttattacgct ttgacgatct 40

<210> SEQ ID NO 26
 <211> LENGTH: 1143
 <212> TYPE: DNA
 <213> ORGANISM: *Aspergillus oryzae*
 <400> SEQUENCE: 26
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 gtcctcatca tcagccagcc ctttgggttc cgcggattga gagagatcgg catcgctgtc 180
 tatatcctca acctgatcct cttcgccctt gtctgctcta ccatggctat aaggttcatc 240
 ctgcacggca accttctgga gtccctccgt catgaccgag agggctctctt cttcccgacc 300
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 aatgagtcct tccaaactagc cctcgaagcc ctcttctgga tctactgcgt ctgcacctta 420
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 atccgctcgc ccccgaggc cttccacctc aactgggtggg ccatggtctt ccccaacacc 960
 ggcttcaccc tggccaccat caccctgggc aaggtcttca acagtaacgg cgtgaagggc 1020

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gtcggctccg ccattgtctat ctgcacgtg tgcattgaca tcttcgtctt tgtaacaat 1080
gtccgcgcgcg ttatccggaa ggatatcatg taccgggga aagatgagga tgtatctgat 1140
tag 1143

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<210> SEQ ID NO 27
<211> LENGTH: 380
<212> TYPE: PRT
<213> ORGANISM: Aspergillus oryzae

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<400> SEQUENCE: 27

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Gly Ile Arg Glu Arg Leu Arg His Phe Thr Trp Ala Trp Tyr Thr Leu
20     25     30
Thr Met Ser Gly Gly Gly Leu Ala Val Leu Ile Ile Ser Gln Pro Phe
35     40     45
Gly Phe Arg Gly Leu Arg Glu Ile Gly Ile Ala Val Tyr Ile Leu Asn
50     55     60
Leu Ile Leu Phe Ala Leu Val Cys Ser Thr Met Ala Ile Arg Phe Ile
65     70     75     80
Leu His Gly Asn Leu Leu Glu Ser Leu Arg His Asp Arg Glu Gly Leu
85     90     95
Phe Phe Pro Thr Phe Trp Leu Ser Val Ala Thr Ile Ile Cys Gly Leu
100    105    110
Ser Arg Tyr Phe Gly Glu Glu Ser Asn Glu Ser Phe Gln Leu Ala Leu
115    120    125
Glu Ala Leu Phe Trp Ile Tyr Cys Val Cys Thr Leu Leu Val Ala Ile
130    135    140
Ile Gln Tyr Ser Phe Val Phe Ser Ser His Lys Tyr Gly Leu Gln Thr
145    150    155    160
Met Met Pro Ser Trp Ile Leu Pro Ala Phe Pro Ile Met Leu Ser Gly
165    170    175
Thr Ile Ala Ser Val Ile Gly Glu Gln Gln Pro Ala Arg Ala Ala Leu
180    185    190
Pro Ile Ile Gly Ala Gly Val Thr Phe Gln Gly Leu Gly Phe Ser Ile
195    200    205
Ser Phe Met Met Tyr Ala His Tyr Ile Gly Arg Leu Met Glu Ser Gly
210    215    220
Leu Pro His Ser Asp His Arg Pro Gly Met Phe Ile Cys Val Gly Pro
225    230    235    240
Pro Ala Phe Thr Ala Leu Ala Leu Val Gly Met Ser Lys Gly Leu Pro
245    250    255
Glu Asp Phe Lys Leu Leu His Asp Ala His Ala Leu Glu Asp Gly Arg
260    265    270
Ile Ile Glu Leu Leu Ala Ile Ser Ala Gly Val Phe Leu Trp Ala Leu
275    280    285
Ser Leu Trp Phe Phe Cys Ile Ala Ile Val Ala Val Ile Arg Ser Pro
290    295    300
Pro Glu Ala Phe His Leu Asn Trp Trp Ala Met Val Phe Pro Asn Thr
305    310    315    320
Gly Phe Thr Leu Ala Thr Ile Thr Leu Gly Lys Ala Leu Asn Ser Asn
325    330    335
Gly Val Lys Gly Val Gly Ser Ala Met Ser Ile Cys Ile Val Cys Met
340    345    350

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Tyr Ile Phe Val Phe Val Asn Asn Val Arg Ala Val Ile Arg Lys Asp
 355 360 365

Ile Met Tyr Pro Gly Lys Asp Glu Asp Val Ser Asp
 370 375 380

<210> SEQ ID NO 28

<211> LENGTH: 1182

<212> TYPE: DNA

<213> ORGANISM: *Aspergillus terreus*

<400> SEQUENCE: 28

```

atgtttgaga acactgcccc tccagggagc tcccgcctcg actctggcat cctggaccat    60
gaattcgaga agcagccggg ttccgtgggc atgcgtgaac gcatccgcca ttttacctgg    120
gacctgtata ctctcacaat gagtgcgtgt ggcttggccc tctctcttgg gagccagcca    180
aacaccttca ccggcctgag ggagattgga ctgcgcgtgt acctgctcaa cctgctcttc    240
tttgcccttg tctgctcgac catggccggc cgggttcacc tgcacggagg gctggctgac    300
tctctccggc acgaacgcga gggcatcttc tccccaacct tctggctctc gatcgccacc    360
atcatcacag gcctgtaccg ctacttcggc gaagacgccg gacgccctt cgtgctcgcc    420
ctcgaagccc tcttctggat ctactgcgct tgcacctcc tctgcgcgt catccaatac    480
tcttggctct tctccggccc caaataccgc ctccaaacgg ccatgccggg ctggatcttc    540
cccgcccttc ctgtcatgct ctctggcacc atcgccctcg tcatcgccga gcagcagccg    600
gccccgcgcg ccattcccat catcgtcgcc ggcaccacct tccagggcct gggcttcttc    660
atcagcatga tcattgaagc ccactacgtc ggcgcctca tggagtccgg cctgcctgtc    720
cgcgagcacc gcccgggcat gttcatcgcc gtcggcccg cggctttcac ggcgctggcc    780
ctcgtcggca tgaccaaggg gctcccgcac gacttcacgc tcatcgccga tgacttcgcc    840
ttcgaggatg cccgcactct gcaagctgtg gcgatcgccg tcggcgtgtt tctctgggcg    900
ctgagtctgt ggttcttttg cattgcggcc attgcctcg tgcgtctccc gccaacggcc    960
tccacactga gctggtgggc catggtcttc cccaacacgg gcttcacctt cgccacgac    1020
aacctgggta cggccctcaa gacgcagggt atccaggggt tggggacggc catgtcgatt    1080
ggaattgtgt ctattttctt gtttgtgttt atcagccatg tgcgggctgt catcaggaaa    1140
gacattatgt atcctgggaa agacgaggat gtggtggagt aa                        1182

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<210> SEQ ID NO 29

<211> LENGTH: 393

<212> TYPE: PRT

<213> ORGANISM: *Aspergillus terreus*

<400> SEQUENCE: 29

Met Phe Glu Asn Thr Ala Pro Pro Gly Ser Ser Arg Ser Asp Ser Gly
 1 5 10 15

Ile Leu Asp His Glu Phe Glu Lys Gln Pro Gly Ser Val Gly Met Arg
 20 25 30

Glu Arg Ile Arg His Phe Thr Trp Ala Trp Tyr Thr Leu Thr Met Ser
 35 40 45

Ala Gly Gly Leu Ala Leu Leu Gly Ser Gln Pro Asn Thr Phe Thr
 50 55 60

Gly Leu Arg Glu Ile Gly Leu Ala Val Tyr Leu Leu Asn Leu Leu Phe
 65 70 75 80

Phe Ala Leu Val Cys Ser Thr Met Ala Gly Arg Phe Ile Leu His Gly

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85								90				95					
Gly	Leu	Val	Asp	Ser	Leu	Arg	His	Glu	Arg	Glu	Gly	Ile	Phe	Phe	Pro		
			100					105					110				
Thr	Phe	Trp	Leu	Ser	Ile	Ala	Thr	Ile	Ile	Thr	Gly	Leu	Tyr	Arg	Tyr		
		115					120					125					
Phe	Gly	Glu	Asp	Ala	Gly	Arg	Pro	Phe	Val	Leu	Ala	Leu	Glu	Ala	Leu		
	130					135					140						
Phe	Trp	Ile	Tyr	Cys	Ala	Cys	Thr	Leu	Leu	Val	Ala	Val	Ile	Gln	Tyr		
145					150					155					160		
Ser	Trp	Leu	Phe	Ser	Gly	Pro	Lys	Tyr	Arg	Leu	Gln	Thr	Ala	Met	Pro		
				165					170					175			
Gly	Trp	Ile	Leu	Pro	Ala	Phe	Pro	Val	Met	Leu	Ser	Gly	Thr	Ile	Ala		
			180					185						190			
Ser	Val	Ile	Ala	Glu	Gln	Gln	Pro	Ala	Arg	Ala	Ala	Ile	Pro	Ile	Ile		
		195					200					205					
Val	Ala	Gly	Thr	Thr	Phe	Gln	Gly	Leu	Gly	Phe	Ser	Ile	Ser	Met	Ile		
	210					215					220						
Met	Tyr	Ala	His	Tyr	Val	Gly	Arg	Leu	Met	Glu	Ser	Gly	Leu	Pro	Cys		
225					230					235					240		
Arg	Glu	His	Arg	Pro	Gly	Met	Phe	Ile	Ala	Val	Gly	Pro	Pro	Ala	Phe		
				245					250					255			
Thr	Ala	Leu	Ala	Leu	Val	Gly	Met	Thr	Lys	Gly	Leu	Pro	His	Asp	Phe		
			260					265						270			
Gln	Leu	Ile	Gly	Asp	Asp	Phe	Ala	Phe	Glu	Asp	Ala	Arg	Ile	Leu	Gln		
		275					280					285					
Leu	Leu	Ala	Ile	Ala	Val	Gly	Val	Phe	Leu	Trp	Ala	Leu	Ser	Leu	Trp		
	290					295					300						
Phe	Phe	Cys	Ile	Ala	Ala	Ile	Ala	Val	Val	Arg	Ser	Pro	Pro	Thr	Ala		
305					310					315					320		
Phe	His	Leu	Ser	Trp	Trp	Ala	Met	Val	Phe	Pro	Asn	Thr	Gly	Phe	Thr		
			325						330					335			
Leu	Ala	Thr	Ile	Asn	Leu	Gly	Thr	Ala	Leu	Lys	Ser	Glu	Gly	Ile	Gln		
			340					345						350			
Gly	Val	Gly	Thr	Ala	Met	Ser	Ile	Gly	Ile	Val	Ser	Ile	Phe	Leu	Phe		
		355					360					365					
Val	Phe	Ile	Ser	His	Val	Arg	Ala	Val	Ile	Arg	Lys	Asp	Ile	Met	Tyr		
	370					375					380						
Pro	Gly	Lys	Asp	Glu	Val	Val	Glu										
385					390												

<210> SEQ ID NO 30

<211> LENGTH: 1317

<212> TYPE: DNA

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 30

atgggagaat tgaaggaaat tctcaagcag cgctaccatg aattgctcga ctggaacgtc	60
aaagcaccoc acgtccctct ctgcagagg ttgaagcatt tcacatgggc gtggttcgcg	120
tgtacgatgg caaccggtgg cgtcggactc atcatcggat ccttcccttt ccgattctac	180
ggactcaaca cgatcgga gattgtgtac atcctccaga ttttctctt ctcttggtc	240
ggctcgtgta tgctcttcag gtccatcaag tatccgtcca caatcaagga ctctggaac	300
catcatctcg agaaactctt cattgcgact tgtctctct cgatttcgac attcatcgat	360

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atgttggcga tctacgccta ccccgacaca ggcgagtggg tgggtgtgggt catccgaatc	420
ctctactaca tctacgtcgc ggtctccttc atttactgtg tgatggcggt cttcacgatac	480
ttcaacaacc acgtctatac cattgaaacc gcctcgctcg catggatcct cctatctctc	540
cctccgatga tctgtggtgt cattgcgggt gcggtgaact ccaccagcc tgcgcaccag	600
ctcaaaaaca tgggtatttt cggaatcctc ttccagggat tgggtttctg ggtctacttg	660
ctcttggtcg cagtcaacgt gctccgggtc ttcacggtcg gcttggcaaa gcccaggac	720
cgacctggca tgttcattgt cgtgggacct cctgcgttct ccggttggc actcatcaac	780
atcgcgaggg gtgccatggg ctgcaggccg tacatcttcg tgggagcaaa ctctcggaa	840
tacttgggtt tctgtctgac gttcatggcg attttcatct ggggcttggc agcatggtgt	900
tattgtctcg ccattggtgc ctctctcgca ggcttcttca caccgcacc ttgaagtgc	960
gcgtgtgggt gggttcgcat catcttcccc aacgtgggct tctgaactg tacgattgag	1020
atcggaaga tgatcgactc caaagccttc cagatgttcg gccacattat cgggtgcatc	1080
ctctgtatcc agtggatttt gctcatgtat ttgatgggc gtgcgttctt ggtcaacgac	1140
ttgtgttacc ccggtaaaga cgaggacgcc catccgcctc ccaaacccaa cacaggcgtc	1200
ctcaacccca ccttccctcc cgaagaaaga cctgcctccc tcgaaaaagt cgatacacat	1260
gtcacttcca ctggcggaga gtcggatcct ccgtcctccg aacacgagtc ggtctaa	1317

<210> SEQ ID NO 31

<211> LENGTH: 1317

<212> TYPE: DNA

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 31

atgggtgaac tcaaggaaat cttgaaacag aggtatcatg agttgcttga ctggaatgtc	60
aaagcccctc atgtccctct cagtcaacga ctgaagcatt ttacatgggc ttggtttgca	120
tgtactatgg caactgggtg tgttggtttg attattggtt ctttccctt tcgattttat	180
ggctttaata caattggcaa aattgtttat attcttcaaa tctttttgtt ttctctctt	240
ggatcatgca tgctttttcg ctttattaaa tatccttcaa ctatcaagga ttctggaac	300
catcatttgg aaaagctttt cattgtact tgtcttctt caatatccac gttcatcgac	360
atgcttgcca tatacgccta tctgatacc ggcgagtggg tgggtgtgggt cattcgaatc	420
ctttattaca ttacgttgc agtatcctt atatactgcg taatggcttt tttacaatt	480
ttcaacaacc atgtatatac cattgaaacc gcatctcctg cttggattct tctattttc	540
cctctatga tttgtggtgt cattgtggc gccgtcaatt ctacacaacc cgtcatcaa	600
ttaaaaaata tggttatctt tggatcctc tttcaaggac ttggtttttg ggtttatctt	660
ttactgtttg ccgtcaatgt cttacgggtt ttactgtag gcctggcaaa accccaagat	720
cgacctggta tgtttatgtt tgcgggtcca ccagcttctc caggtttggc cttaattaat	780
attgcgctg gtgctatggg cagtcgcct tatatttttg ttggcgccaa ctcatccgag	840
tatcttgggt ttgtttctac ctttatggct atttttattt ggggtcttgc tgcctggtgt	900
tactgtctcg ccattggttag ctttttagcg ggcttttcca ctcgagcccc tctcaagttt	960
gcttgggtat gggttgcatt cattttcccc aacgtgggtt ttgttaattg taccattgag	1020
ataggtaaaa tgatagattc caaagcttcc caaatgtttg gacatatcat tggggtcatt	1080
ctttgtatcc agtggatcct cctaatgtat ttaatggccc gtgcgttctc cgtcaatgat	1140
ctttgctatc ctggcaaaaga cgaagatgcc catcctccac caaaacccaa tacaggtgtc	1200

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cttaacccta ccttcccacc tgaaaaagca cctgcatctt tggaaaaagt cgatacacat 1260
gtcacatcta ctggtggtga atcggtatcct cctagtagtg aacatgaaag cgttttaa 1317

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<210> SEQ ID NO 32

<211> LENGTH: 438

<212> TYPE: PRT

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 32

```

Met Gly Glu Leu Lys Glu Ile Leu Lys Gln Arg Tyr His Glu Leu Leu
 1           5           10          15
Asp Trp Asn Val Lys Ala Pro His Val Pro Leu Ser Gln Arg Leu Lys
 20          25          30
His Phe Thr Trp Ser Trp Phe Ala Cys Thr Met Ala Thr Gly Gly Val
 35          40          45
Gly Leu Ile Ile Gly Ser Phe Pro Phe Arg Phe Tyr Gly Leu Asn Thr
 50          55          60
Ile Gly Lys Ile Val Tyr Ile Leu Gln Ile Phe Leu Phe Ser Leu Phe
 65          70          75          80
Gly Ser Cys Met Leu Phe Arg Phe Ile Lys Tyr Pro Ser Thr Ile Lys
 85          90          95
Asp Ser Trp Asn His His Leu Glu Lys Leu Phe Ile Ala Thr Cys Leu
100          105          110
Leu Ser Ile Ser Thr Phe Ile Asp Met Leu Ala Ile Tyr Ala Tyr Pro
115          120          125
Asp Thr Gly Glu Trp Met Val Trp Val Ile Arg Ile Leu Tyr Tyr Ile
130          135          140
Tyr Val Ala Val Ser Phe Ile Tyr Cys Val Met Ala Phe Phe Thr Ile
145          150          155          160
Phe Asn Asn His Val Tyr Thr Ile Glu Thr Ala Ser Pro Ala Trp Ile
165          170          175
Leu Pro Ile Phe Pro Pro Met Ile Cys Gly Val Ile Ala Gly Ala Val
180          185          190
Asn Ser Thr Gln Pro Ala His Gln Leu Lys Asn Met Val Ile Phe Gly
195          200          205
Ile Leu Phe Gln Gly Leu Gly Phe Trp Val Tyr Leu Leu Leu Phe Ala
210          215          220
Val Asn Val Leu Arg Phe Phe Thr Val Gly Leu Ala Lys Pro Gln Asp
225          230          235          240
Arg Pro Gly Met Phe Met Phe Val Gly Pro Pro Ala Phe Ser Gly Leu
245          250          255
Ala Leu Ile Asn Ile Ala Arg Gly Ala Met Gly Ser Arg Pro Tyr Ile
260          265          270
Phe Val Gly Ala Asn Ser Ser Glu Tyr Leu Gly Phe Val Ser Thr Phe
275          280          285
Met Ala Ile Phe Ile Trp Gly Leu Ala Ala Trp Cys Tyr Cys Leu Ala
290          295          300
Met Val Ser Phe Leu Ala Gly Phe Phe Thr Arg Ala Pro Leu Lys Phe
305          310          315          320
Ala Cys Gly Trp Phe Ala Phe Ile Phe Pro Asn Val Gly Phe Val Asn
325          330          335
Cys Thr Ile Glu Ile Gly Lys Met Ile Asp Ser Lys Ala Phe Gln Met
340          345          350

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Phe Gly His Ile Ile Gly Val Ile Leu Cys Ile Gln Trp Ile Leu Leu
355 360 365

Met Tyr Leu Met Val Arg Ala Phe Leu Val Asn Asp Leu Cys Tyr Pro
370 375 380

Gly Lys Asp Glu Asp Ala His Pro Pro Pro Lys Pro Asn Thr Gly Val
385 390 395 400

Leu Asn Pro Thr Phe Pro Pro Glu Lys Ala Pro Ala Ser Leu Glu Lys
405 410 415

Val Asp Thr His Val Thr Ser Thr Gly Gly Glu Ser Asp Pro Pro Ser
420 425 430

Ser Glu His Glu Ser Val
435

<210> SEQ ID NO 33
<211> LENGTH: 1194
<212> TYPE: DNA
<213> ORGANISM: *Aspergillus aculeatus*

<400> SEQUENCE: 33

atgctcgggc aacatccgcc tcccacaccc tctgctcgg accttacaac ataccagcat	60
gagctcaaag cctccaaata ctctagttcc accaatgtgt ctctacggga cgtctgcgt	120
cattttacct gggcgtggta tactctgact atgagcaccg gcggtctagc cctcctgctg	180
gccagccagc cctactcett ctccggactg caacagateg ggcttgagc ctacatcatc	240
aacctggcct tctttgcgtt gctgtgtagc ctcatggcgg cagcgttcat tctccacggc	300
aacttcctcg actccctcgg acacgaccgc gaggggtctt tctttcctac tttctggctt	360
tctattgcaa ctatcatcac cggcctgtac cgctacttcg gcgacaccac acagcctgca	420
ttcatttaag ctcttgaggt gctcttctgg ctctactgtg ccttcaactct gatgaccgct	480
attatccaat actcctttgt ctttacgcc caccactacc ctctacaaac gatgatgccc	540
tcattggatcc tccccgcatt cctatcatg ctacagcgca cgatcgctc cgtaattgcc	600
gaacagcagc ccgcgcgctc tgetattccc atgatcgctg ccggcaccac cttccaaggc	660
cttggtctct ccatcagttt cctcatgtac gcgcactata tcgggcgggt catggagacg	720
ggccttcctg cccgggaaca ccgaccggg atgttcatct gcgttgcccc cccggctttc	780
acggcccttg ccctaateg catgaccaac ggcttctctg aggatattca agtcttcaa	840
gaccgcacc cctttcaaga cgcgcacatc ctccgactcc ttgcatcgcc cagggcgccc	900
ttcctctggg ccctcagttc ctgggtcttt agcattgcca tcatcgccac catccgcctc	960
ccacctacag ccttccacct caactgggtg gccatgggtt ttccaaacac gggttttact	1020
ctcgcgacca tcacgctggg caaagccttc gatagccctg gattcaaggg cgtcggatct	1080
gccatgtcca tttgcatcgt ggggatgtgg ctgttcgtgt ttgcgagcaa tatccgtgcc	1140
gttgtcaaac gggatattgt tttccctggg aaggacgagg atgtatcgga gtaa	1194

<210> SEQ ID NO 34
<211> LENGTH: 397
<212> TYPE: PRT
<213> ORGANISM: *Aspergillus aculeatus*

<400> SEQUENCE: 34

Met Leu Gly Gln His Pro Pro Pro Asp Thr Ser Cys Ser Asp Leu Thr
1 5 10 15

Thr Tyr Gln His Glu Leu Lys Ala Ser Lys Tyr Ser Ser Ser Thr Asn
20 25 30

-continued

Val Ser Leu Arg Asp Arg Leu Arg His Phe Thr Trp Ala Trp Tyr Thr
 35 40 45
 Leu Thr Met Ser Thr Gly Gly Leu Ala Leu Leu Leu Ala Ser Gln Pro
 50 55 60
 Tyr Ser Phe Ser Gly Leu Gln Gln Ile Gly Leu Ala Val Tyr Ile Ile
 65 70 75 80
 Asn Leu Ala Phe Phe Ala Leu Leu Cys Ser Leu Met Ala Ala Arg Phe
 85 90 95
 Ile Leu His Gly Asn Phe Leu Asp Ser Leu Arg His Asp Arg Glu Gly
 100 105 110
 Leu Phe Phe Pro Thr Phe Trp Leu Ser Ile Ala Thr Ile Ile Thr Gly
 115 120 125
 Leu Tyr Arg Tyr Phe Gly Asp Thr Thr Gln Pro Ala Phe Ile Tyr Ala
 130 135 140
 Leu Glu Val Leu Phe Trp Leu Tyr Cys Ala Phe Thr Leu Met Thr Ala
 145 150 155 160
 Ile Ile Gln Tyr Ser Phe Val Phe Thr Ala His His Tyr Pro Leu Gln
 165 170 175
 Thr Met Met Pro Ser Trp Ile Leu Pro Ala Phe Pro Ile Met Leu Ser
 180 185 190
 Gly Thr Ile Ala Ser Val Ile Ala Glu Gln Gln Pro Ala Arg Ser Ala
 195 200 205
 Ile Pro Met Ile Val Ala Gly Thr Thr Phe Gln Gly Leu Gly Phe Ser
 210 215 220
 Ile Ser Phe Leu Met Tyr Ala His Tyr Ile Gly Arg Leu Met Glu Thr
 225 230 235 240
 Gly Leu Pro Ser Arg Glu His Arg Pro Gly Met Phe Ile Cys Val Gly
 245 250 255
 Pro Pro Ala Phe Thr Ala Leu Ala Leu Ile Gly Met Thr Asn Gly Leu
 260 265 270
 Pro Glu Asp Phe Gln Val Leu Gln Asp Pro His Pro Phe Gln Asp Ala
 275 280 285
 His Ile Leu Arg Leu Leu Ala Ile Ala Thr Gly Ala Phe Leu Trp Ala
 290 295 300
 Leu Ser Leu Trp Phe Phe Ser Ile Ala Ile Ile Ala Thr Ile Arg Leu
 305 310 315 320
 Pro Pro Thr Ala Phe His Leu Asn Trp Trp Ala Met Val Phe Pro Asn
 325 330 335
 Thr Gly Phe Thr Leu Ala Thr Ile Thr Leu Gly Lys Ala Phe Asp Ser
 340 345 350
 Pro Gly Val Lys Gly Val Gly Ser Ala Met Ser Ile Cys Ile Val Gly
 355 360 365
 Met Trp Leu Phe Val Phe Ala Ser Asn Ile Arg Ala Val Val Lys Arg
 370 375 380
 Asp Ile Val Phe Pro Gly Lys Asp Glu Asp Val Ser Glu
 385 390 395

<210> SEQ ID NO 35

<211> LENGTH: 1194

<212> TYPE: DNA

<213> ORGANISM: Aspergillus aculeatus

<400> SEQUENCE: 35

atgctcgggc aacactcgcc tcccggcacc tcctgctcgg accttacaac ataccaacat

60

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gagcttaaag cctccaaata ctctagttcc accaatgtgt ctctacggga cegtctgcgt 120
cattttacct gggcctggta tactctgact atgagcaccg gcggcctagc gcttctgctg 180
gccagccagc cctacacctt ctccggactg caacagatcg ggcttgcaat ctatatcatc 240
aacctgggtc tctttgcttt gctgtgcagc ctcatggcca cgcgcttcat tctccacggc 300
aacttcctcg actccctcgg acacgaccgc gaggggtcttt tctttccac tttctggctt 360
tccattgcaa ctatcatcac cggactctac cgctacttcg gcgacaccac acagcctgca 420
ttcatttacg cccttgaggt gcttttctgg ctctactgtg ccttcacact gatgaccgct 480
atcatccaat actcttttgt ctttactgcc caccactacc ctctacaaac gatgatgccc 540
tcgtggatcc tccccgcatt ccccatcatg ctaagcgga cgatgcgctc tgctattgcc 600
gaacagcagc ccgcgcgctc tgctattccc atgatcgctg ccggcaccac cttccaaggc 660
cttggtctct ccacagttt cctcatgtac gcgcactata tcggacgctt catggagacg 720
ggccttccgt cccgggaaca ccgaccggg atgttcatct gcgttgccc cctgctttc 780
acggcccttg ccctaategg catgaccaac ggccttctcg aggattttca agtcttcaa 840
gacccgcacc ctttcaaga cgcgcatatc ctccgactcc ttgccatgc cagggcgcc 900
ttcctctggg ccctcagttc ctggttcttc agcattgcca ttatgcgac catccgctc 960
ccacctacgg ccttccacct caactgggtg gccatggttt ttccaaacac gggttttact 1020
ctcgcgacca tcacgctggg caaagccttc gatagccctg gagtcaaggg cgtcggatct 1080
gccatgtcca tttgatcgt ggggatgtgg ctgttcgtgt ttgcgagcaa tatccgcgcc 1140
gttgtcaaac gggatattgt gtttctggc aaggacgagg atgtatcgga gtaa 1194

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<210> SEQ ID NO 36

<211> LENGTH: 397

<212> TYPE: PRT

<213> ORGANISM: Aspergillus aculeatus

<400> SEQUENCE: 36

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Met Leu Gly Gln His Ser Pro Pro Gly Thr Ser Cys Ser Asp Leu Thr
1           5           10           15
Thr Tyr Gln His Glu Leu Lys Ala Ser Lys Tyr Ser Ser Ser Thr Asn
20          25          30
Val Ser Leu Arg Asp Arg Leu Arg His Phe Thr Trp Ala Trp Tyr Thr
35          40          45
Leu Thr Met Ser Thr Gly Gly Leu Ala Leu Leu Leu Ala Ser Gln Pro
50          55          60
Tyr Thr Phe Ser Gly Leu Gln Gln Ile Gly Leu Ala Val Tyr Ile Ile
65          70          75          80
Asn Leu Val Phe Phe Ala Leu Leu Cys Ser Leu Met Ala Thr Arg Phe
85          90          95
Ile Leu His Gly Asn Phe Leu Asp Ser Leu Arg His Asp Arg Glu Gly
100         105         110
Leu Phe Phe Pro Thr Phe Trp Leu Ser Ile Ala Thr Ile Ile Thr Gly
115         120         125
Leu Tyr Arg Tyr Phe Gly Asp Thr Thr Gln Pro Ala Phe Ile Tyr Ala
130         135         140
Leu Glu Val Leu Phe Trp Leu Tyr Cys Ala Phe Thr Leu Met Thr Ala
145         150         155         160
Ile Ile Gln Tyr Ser Phe Val Phe Thr Ala His His Tyr Pro Leu Gln
165         170         175

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Thr Met Met Pro Ser Trp Ile Leu Pro Ala Phe Pro Ile Met Leu Ser
 180 185 190
 Gly Thr Ile Ala Ser Val Ile Ala Glu Gln Gln Pro Ala Arg Ser Ala
 195 200 205
 Ile Pro Met Ile Val Ala Gly Thr Thr Phe Gln Gly Leu Gly Phe Ser
 210 215 220
 Ile Ser Phe Leu Met Tyr Ala His Tyr Ile Gly Arg Leu Met Glu Thr
 225 230 235 240
 Gly Leu Pro Ser Arg Glu His Arg Pro Gly Met Phe Ile Cys Val Gly
 245 250 255
 Pro Pro Ala Phe Thr Ala Leu Ala Leu Ile Gly Met Thr Asn Gly Leu
 260 265 270
 Pro Glu Asp Phe Gln Val Leu Gln Asp Pro His Pro Phe Gln Asp Ala
 275 280 285
 His Ile Leu Arg Leu Leu Ala Ile Ala Thr Gly Ala Phe Leu Trp Ala
 290 295 300
 Leu Ser Leu Trp Phe Phe Ser Ile Ala Ile Ile Ala Thr Ile Arg Leu
 305 310 315 320
 Pro Pro Thr Ala Phe His Leu Asn Trp Trp Ala Met Val Phe Pro Asn
 325 330 335
 Thr Gly Phe Thr Leu Ala Thr Ile Thr Leu Gly Lys Ala Phe Asp Ser
 340 345 350
 Pro Gly Val Lys Gly Val Gly Ser Ala Met Ser Ile Cys Ile Val Gly
 355 360 365
 Met Trp Leu Phe Val Phe Ala Ser Asn Ile Arg Ala Val Val Lys Arg
 370 375 380
 Asp Ile Val Phe Pro Gly Lys Asp Glu Asp Val Ser Glu
 385 390 395

<210> SEQ ID NO 37

<211> LENGTH: 1353

<212> TYPE: DNA

<213> ORGANISM: Schizosaccharomyces japonicus

<400> SEQUENCE: 37

atgtcgtcgg agacaccgac atactcctcc tgggcatccc agaggtacaa cgaattgatt 60
 gcatggaacg tcaaggtgcc gaggttgccc atcgcacaga ggctcaagca cttcactgtg 120
 tcgtggttca cgtgtactat ggcaacaggc ggtgtcggaa tgatcctcgc gtcgtcctcc 180
 tatagggtca cgggcttgaa caccatcgga aaggctcgtc tcattttcca ggtggtcttg 240
 ttggccatct tctgttcggc catggccttc aggttcattc gctacccgga gactttcaag 300
 aagtcgatct atcaccactt ggagaaattg ttcacgggta cattcttgcg ctgatgtcgc 360
 acctcatcg atatgctcgc agcctacggc tacccttcca ccggtgaatg gatggtgtac 420
 ttgatccgaa tcttctactg gatgtacttc gccgtctcct tcgtctacgc gatcttcgca 480
 ttcgcaacta ctttccatat gcatccttat accctcgaaa cggcatcgcc tgctgggac 540
 ctcccgattt tcctcgcat gatctccgga gcagtggcag gaaccgtggc attcactcag 600
 cctccccatc agctcaaaaa cctcgtggtg tgttggeatta tgttcacagg tttgggcttc 660
 tgggtctaca tcatgttggt cgcgggtcaac atgctcaaat tgttcacaaa gggcatgatg 720
 ggagcctcgg aacgaccggg tttgttcatg ttcgtcggac ctccggcata cacaggcctc 780
 gccctcatcg gtatgggcaa gaccgcatg gattccaaaa tctccatggt ctccgccact 840

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cccgctctcct ccgaacacct cgcattcatg tgtaccttca tggcactctt catgtgggggt    900
ctcgcagcgt ggtgttattg tgtggcgatg gtctgtttcg cagcaggttt catgtccagg    960
gcacctatcc agttcaagtt gggatgggtc gcgttcacat tccctgtcgt gggcttcgtg    1020
aacgtcacca tgaagatcgg cgagatgatt gactcggcag ccttcaaaat ctteggecac    1080
gtcatcggag ccatgttggc catccagtgg atgttcgtga tgtttctcat ggtgcgagcg    1140
gtcttgttgc aggaatcat gtatcctgga cgggacgagg acgtcaaaac accgcctgga    1200
gccacacctc ctccgacctc cgtgacctcc cctctctcct tcgcacctcc ccaggatgtc    1260
aaggatggac accccatcca ggtgacggtc tcccgcacta gggatcggtc gaaacagcac    1320
atgtcccagg gctcggacga ggaaaagatt taa                                     1353

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<210> SEQ ID NO 38
<211> LENGTH: 1353
<212> TYPE: DNA
<213> ORGANISM: Schizosaccharomyces japonicus

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<400> SEQUENCE: 38

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atgtcttcgg aaacgccgac ttacagctct tgggcgagcc aacggtacaa cgaattgatc    60
gcttggaacg tcaagggtec tcgcttacct attgcccagc gtctaaaaca cttcacttgg    120
tcttggttta cctgtacctt ggcacccggt ggtgtcggta tgattctggc atcgtgccc    180
taccgattca caggcttaaa cagcattggt aaagtctgtt tcattttcca ggtcgttttg    240
ctggcgattt tctgttcggc gatggccttt cggttcattc gttacccga aaccttcaaa    300
aagtctatct accatcatct ggagaagctc ttcattggta cttctctgct ttccatgtcg    360
acgttcacgc atatgctcgc cgctacgga taccacgca ctggcgagtg gatgggtgac    420
ctaattcgca ttttttactg gatgtacttt gccgtctcgt tcgtatacgc catcttcgca    480
tttgctacca cttttcacat gcacccctac accctggaga cggcttcccc agcatggatt    540
ctgcctatct tcccagctat gattagcggc gctgtcgcgc gtactgtggc ctccacacaa    600
ccgcgcgacc aattgaagaa tttggctcgt tgcggtatca tgttccaggc cttgggtttc    660
tgggtgtaca tcatgctgtt cgcctgaac atgctcaagc tgtttacgaa gggatatgatg    720
ggtgcctctg aacgccctgg tctttttatg ttcgttggtc ctccggccta tacggccttg    780
gctttaatcg gtatgggtaa aactgctatg gactccaaga tctccatggt ttctgcaacc    840
cccgtttctt ctgaacacct tgcctttatg tgtaccttta tggccttggt tatgtgggggt    900
cttgctgctt ggtgctattg tgtggccatg gtctgctttg ctgctgggtt catgtctcgt    960
gctctatctc aattcaaaact cggtcgggtc gcatttattt tcccagtcgt tggttttgtc    1020
aacgttacta tgaagattgg tgagatgatt gattcggccg cgttcaagat ctttggatcat    1080
gtcattgggt caatgcttgc cattcagtgg atgtttgtga tgtttctcat ggtccgcgcc    1140
gtcttactgc aagagatcat gtaccggggc cgcgacgaag atgtcaagac acctcccgggt    1200
gccactctc ctcccacttt ggtgacgagt ccttgcctct ttgcttcgct gcaagacgta    1260
aaagatggcc atcccatcca ggtcaccggt tcccgcactc gagacagaag caaacagcac    1320
atgtcgcagg gctctgatga agaaaaaatc tag                                     1353

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<210> SEQ ID NO 39
<211> LENGTH: 450
<212> TYPE: PRT
<213> ORGANISM: Schizosaccharomyces japonicus

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<400> SEQUENCE: 39

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Met	Ser	Ser	Glu	Thr	Pro	Thr	Tyr	Ser	Ser	Trp	Ala	Ser	Gln	Arg	Tyr
1				5				10					15		
Asn	Glu	Leu	Ile	Ala	Trp	Asn	Val	Lys	Gly	Pro	Arg	Leu	Pro	Ile	Ala
		20						25				30			
Gln	Arg	Leu	Lys	His	Phe	Thr	Trp	Ser	Trp	Phe	Thr	Cys	Thr	Met	Ala
		35					40					45			
Thr	Gly	Gly	Val	Gly	Met	Ile	Leu	Ala	Ser	Leu	Pro	Tyr	Arg	Phe	Thr
	50					55					60				
Gly	Leu	Asn	Thr	Ile	Gly	Lys	Val	Val	Phe	Ile	Phe	Gln	Val	Val	Leu
65					70					75					80
Leu	Ala	Ile	Phe	Cys	Ser	Ala	Met	Ala	Phe	Arg	Phe	Ile	Arg	Tyr	Pro
			85						90					95	
Glu	Thr	Phe	Lys	Lys	Ser	Ile	Tyr	His	His	Leu	Glu	Lys	Leu	Phe	Ile
			100					105					110		
Gly	Thr	Phe	Leu	Leu	Ser	Met	Ser	Thr	Phe	Ile	Asp	Met	Leu	Ala	Ala
			115					120				125			
Tyr	Gly	Tyr	Pro	Ser	Thr	Gly	Glu	Trp	Met	Val	Tyr	Leu	Ile	Arg	Ile
	130					135					140				
Phe	Tyr	Trp	Met	Tyr	Phe	Ala	Val	Ser	Phe	Val	Tyr	Ala	Ile	Phe	Ala
145					150					155					160
Phe	Ala	Thr	Thr	Phe	His	Met	His	Pro	Tyr	Thr	Leu	Glu	Thr	Ala	Ser
				165					170					175	
Pro	Ala	Trp	Ile	Leu	Pro	Ile	Phe	Pro	Ala	Met	Ile	Ser	Gly	Ala	Val
			180					185					190		
Ala	Gly	Thr	Val	Ala	Phe	Thr	Gln	Pro	Pro	His	Gln	Leu	Lys	Asn	Leu
			195				200					205			
Val	Val	Cys	Gly	Ile	Met	Phe	Gln	Gly	Leu	Gly	Phe	Trp	Val	Tyr	Ile
	210					215					220				
Met	Leu	Phe	Ala	Val	Asn	Met	Leu	Lys	Leu	Phe	Thr	Lys	Gly	Met	Met
225					230					235				240	
Gly	Ala	Ser	Glu	Arg	Pro	Gly	Leu	Phe	Met	Phe	Val	Gly	Pro	Pro	Ala
				245					250					255	
Tyr	Thr	Gly	Leu	Ala	Leu	Ile	Gly	Met	Gly	Lys	Thr	Ala	Met	Asp	Ser
		260						265						270	
Lys	Ile	Ser	Met	Phe	Ser	Ala	Thr	Pro	Val	Ser	Ser	Glu	His	Leu	Ala
		275					280						285		
Phe	Met	Cys	Thr	Phe	Met	Ala	Leu	Phe	Met	Trp	Gly	Leu	Ala	Ala	Trp
	290					295					300				
Cys	Tyr	Cys	Val	Ala	Met	Val	Cys	Phe	Ala	Ala	Gly	Phe	Met	Ser	Arg
305					310					315					320
Ala	Pro	Ile	Gln	Phe	Lys	Leu	Gly	Trp	Phe	Ala	Phe	Ile	Phe	Pro	Val
				325					330					335	
Val	Gly	Phe	Val	Asn	Val	Thr	Met	Lys	Ile	Gly	Glu	Met	Ile	Asp	Ser
			340					345					350		
Ala	Ala	Phe	Lys	Ile	Phe	Gly	His	Val	Ile	Gly	Ala	Met	Leu	Ala	Ile
			355				360					365			
Gln	Trp	Met	Phe	Val	Met	Phe	Phe	Met	Val	Arg	Ala	Val	Leu	Leu	Gln
	370					375					380				
Glu	Ile	Met	Tyr	Pro	Gly	Arg	Asp	Glu	Asp	Val	Lys	Thr	Pro	Pro	Gly
385					390					395					400
Ala	Thr	Pro	Pro	Pro	Thr	Leu	Val	Thr	Ser	Pro	Leu	Ser	Phe	Ala	Ser
				405					410					415	

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Leu Gln Asp Val Lys Asp Gly His Pro Ile Gln Val Thr Val Ser Arg
420 425 430

Thr Arg Asp Arg Ser Lys Gln His Met Ser Gln Gly Ser Asp Glu Glu
435 440 445

Lys Ile
450

<210> SEQ ID NO 40
<211> LENGTH: 1179
<212> TYPE: DNA
<213> ORGANISM: *Aspergillus clavatus*

<400> SEQUENCE: 40

```

atgttcgaaa atcgataacc gccgacctcg tctcagtcag actctggctt cctcgagaac    60
cagctggaaa aacaacatcg actcagcctc cgtgagaggt taaggcactt tacctgggcc    120
tggtacacat tgaccatgag cacaggtggg ttggctctcc tgatagcgag ccagccatac    180
accttcaagg ggttgaagac cattggactg gtggctctaca tcgtgaactt gatcttgttt    240
ggctctgtct gttcccttat ggccactagg ttcactctcc acggtggctt cctcgactcc    300
cttcgccatg agcgcgaggg tcttttcttt cctaccttct ggctatccgt agcaaccatc    360
atcacgggct tgcacgcta cttcggtccc gatgctcgag aatcgtaact gattgcactc    420
gaagtactct tctgggtcta ctgtgcctgt acaactggcca cagcagtgat ccagtactcc    480
ttcatcttct ctgcgcacag atacggcctc cagaccatga tgccctcctg gattctccca    540
gccttcccca tcatgctcag tggcacgatt gcctcgtca tcggcgaagc tcaaccgcga    600
cggctcatga tccccgctcat catggccgga gtcaccttcc agggcctggg gttctcgatc    660
agcttcatga tgtacgcca ctatatcggc cggctgatgg aatcagggct cccctgccgc    720
gagcacagac ccggcatggt catctgcgtt ggtcccccg ctttcacagc cctcgctcta    780
gtcgggatgg ccaagggcct gcccgccgag ttcaaagctca tcaacgacgc acacgcctc    840
gaagacgcgc ggatcctoga gctgctogca atcacgcgg gcatottcct ctgggccttg    900
agtctgtggt tcttcttcat cgcgctcact gccgtcctcc gggtcccgcc tacttctctc    960
catctcaact ggtgggcctt ggtcttcccg aacacgggct tcactttggc caccatcacg   1020
cttggaagg cattgggcag tcccgggac ttgggcgttg gttctgccat gtcccttggc   1080
atcgttggca tgtggctggt tgtttttgtc agccatatcc gtgccatcat caaccaggat   1140
atcatgtatc cgggcaaaga tgaggatgct gcagactag                               1179

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<210> SEQ ID NO 41
<211> LENGTH: 392
<212> TYPE: PRT
<213> ORGANISM: *Aspergillus clavatus*

<400> SEQUENCE: 41

Met Phe Glu Asn Arg Ile Pro Pro Thr Ser Ser Gln Ser Asp Ser Gly
1 5 10 15

Phe Leu Glu Asn Gln Leu Glu Lys Gln His Arg Leu Ser Leu Arg Glu
20 25 30

Arg Leu Arg His Phe Thr Trp Ala Trp Tyr Thr Leu Thr Met Ser Thr
35 40 45

Gly Gly Leu Ala Leu Leu Ile Ala Ser Gln Pro Tyr Thr Phe Lys Gly
50 55 60

Leu Lys Thr Ile Gly Leu Val Val Tyr Ile Val Asn Leu Ile Leu Phe
65 70 75 80

-continued

Gly Leu Val Cys Ser Leu Met Ala Thr Arg Phe Ile Leu His Gly Gly
 85 90 95
 Phe Leu Asp Ser Leu Arg His Glu Arg Glu Gly Leu Phe Phe Pro Thr
 100 105 110
 Phe Trp Leu Ser Val Ala Thr Ile Ile Thr Gly Leu His Arg Tyr Phe
 115 120 125
 Gly Ser Asp Ala Arg Glu Ser Tyr Leu Ile Ala Leu Glu Val Leu Phe
 130 135 140
 Trp Val Tyr Cys Ala Cys Thr Leu Ala Thr Ala Val Ile Gln Tyr Ser
 145 150 155 160
 Phe Ile Phe Ser Ala His Arg Tyr Gly Leu Gln Thr Met Met Pro Ser
 165 170 175
 Trp Ile Leu Pro Ala Phe Pro Ile Met Leu Ser Gly Thr Ile Ala Ser
 180 185 190
 Val Ile Gly Glu Ala Gln Pro Ala Arg Ser Ser Ile Pro Val Ile Met
 195 200 205
 Ala Gly Val Thr Phe Gln Gly Leu Gly Phe Ser Ile Ser Phe Met Met
 210 215 220
 Tyr Ala His Tyr Ile Gly Arg Leu Met Glu Ser Gly Leu Pro Cys Arg
 225 230 235 240
 Glu His Arg Pro Gly Met Phe Ile Cys Val Gly Pro Pro Ala Phe Thr
 245 250 255
 Ala Leu Ala Leu Val Gly Met Ala Lys Gly Leu Pro Ala Glu Phe Lys
 260 265 270
 Leu Ile Asn Asp Ala His Ala Leu Glu Asp Ala Arg Ile Leu Glu Leu
 275 280 285
 Leu Ala Ile Thr Ala Gly Ile Phe Leu Trp Ala Leu Ser Leu Trp Phe
 290 295 300
 Phe Phe Ile Ala Val Ile Ala Val Leu Arg Ser Pro Pro Thr Ser Phe
 305 310 315 320
 His Leu Asn Trp Trp Ala Leu Val Phe Pro Asn Thr Gly Phe Thr Leu
 325 330 335
 Ala Thr Ile Thr Leu Gly Lys Ala Leu Gly Ser Pro Gly Ile Leu Gly
 340 345 350
 Val Gly Ser Ala Met Ser Leu Gly Ile Val Gly Met Trp Leu Phe Val
 355 360 365
 Phe Val Ser His Ile Arg Ala Ile Ile Asn Gln Asp Ile Met Tyr Pro
 370 375 380
 Gly Lys Asp Glu Asp Ala Ala Asp
 385 390

<210> SEQ ID NO 42

<211> LENGTH: 1182

<212> TYPE: DNA

<213> ORGANISM: *Aspergillus fumigatus*

<400> SEQUENCE: 42

atgttcaacg atcatgatca tgttccacca acatcatcac agtcggattc tggctttttt	60
gaacaagaaa tgaagaaatc tctctgacta agccttcgtg agcgectacg gcacttcacc	120
tgggcgtggt ataccttgac gatgagtacc ggtggactgg ctcttctgat tgctagttag	180
ccgtatacct tcaatggcat gaagggcatc gggatggctg tttatatact caatcttctg	240
ttattcgctc ttgtctgttc tttgatggtg ctgagattcg ttttgcattg cggtttccct	300

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gacagcttgc gccaccctcg cgagggtctc ttcttcctca ccttctgggt atccattgca 360
acgatcatca ctggcttgca tcgttacttc ggctccgacg acctagagtc gtacctcatc 420
gcactcgaag tcctctcttg ggtctactgt agttgcaccc tcgccacagc tgtgatccag 480
tactcattec tctttgccgc ccactccctac ggctgcaga caatgatgcc atcatggatc 540
ctaccagcct tccccatcat gctcagcgga accatcgctt cggtcacag cgaatcccag 600
cccgcgcat ccgcatccc catcatcact gccggcggtta ccttcagggt cctcggttc 660
tcaatcagct tcataatgta cgcccactac atcgccgac tcatgcagtc agggcttccc 720
tgccgcgaac acagaccagc catgttcatt tgcgtggggc ctccgtcttt caccgcgttg 780
gcgctagtag ggatggccaa gggcctgccc gacgaattca agataatcaa agacgcacac 840
gtcaggagcg cccggatcct cgagctgatg gctattatcg tcggcgtgtt cctgtggggc 900
ctgagtctct ggttctctct cattgccttt gttgctgctg tccgggtgcc gcccaactgcg 960
ttccacctta gctgggtggg catggtcttc cccaacactg ggttcacgct ggccactatt 1020
accctgggga gggcattggg gagccctggc gtcttggggc tcggctcggc catgtcggtc 1080
ggtgttgtct gcattgtggg ctctgttttc gtctaccaca ttctgtctgt catcaggcaa 1140
gacatcatgt acccgggcaa agacgaggat gtgctagatt aa 1182

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<210> SEQ ID NO 43
<211> LENGTH: 393
<212> TYPE: PRT
<213> ORGANISM: Aspergillus fumigatus

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<400> SEQUENCE: 43

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Met Phe Asn Asp His Asp His Val Pro Pro Thr Ser Ser Gln Ser Asp
1      5      10      15
Ser Gly Phe Phe Glu Gln Glu Met Lys Lys Ser Pro Arg Leu Ser Leu
20     25     30
Arg Glu Arg Leu Arg His Phe Thr Trp Ala Trp Tyr Thr Leu Thr Met
35     40     45
Ser Thr Gly Gly Leu Ala Leu Leu Ile Ala Ser Gln Pro Tyr Thr Phe
50     55     60
Asn Gly Met Lys Gly Ile Gly Met Val Val Tyr Ile Leu Asn Leu Leu
65     70     75     80
Leu Phe Ala Leu Val Cys Ser Leu Met Val Leu Arg Phe Val Leu His
85     90     95
Gly Gly Phe Leu Asp Ser Leu Arg His Pro Arg Glu Gly Leu Phe Phe
100    105    110
Pro Thr Phe Trp Leu Ser Ile Ala Thr Ile Ile Thr Gly Leu His Arg
115    120    125
Tyr Phe Gly Ser Asp Asp Leu Glu Ser Tyr Leu Ile Ala Leu Glu Val
130    135    140
Leu Phe Trp Val Tyr Cys Ser Cys Thr Leu Ala Thr Ala Val Ile Gln
145    150    155    160
Tyr Ser Phe Leu Phe Ala Ala His Ser Tyr Gly Leu Gln Thr Met Met
165    170    175
Pro Ser Trp Ile Leu Pro Ala Phe Pro Ile Met Leu Ser Gly Thr Ile
180    185    190
Ala Ser Val Ile Ser Glu Ser Gln Pro Ala Arg Ser Ala Ile Pro Ile
195    200    205
Ile Thr Ala Gly Val Thr Phe Gln Gly Leu Gly Phe Ser Ile Ser Phe
210    215    220

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Ile Met Tyr Ala His Tyr Ile Gly Arg Leu Met Gln Ser Gly Leu Pro
 225 230 235 240
 Cys Arg Glu His Arg Pro Ala Met Phe Ile Cys Val Gly Pro Pro Ser
 245 250 255
 Phe Thr Ala Leu Ala Leu Val Gly Met Ala Lys Gly Leu Pro Asp Glu
 260 265 270
 Phe Lys Ile Ile Lys Asp Ala His Val Glu Asp Ala Arg Ile Leu Glu
 275 280 285
 Leu Met Ala Ile Ile Val Gly Val Phe Leu Trp Ala Leu Ser Leu Trp
 290 295 300
 Phe Phe Phe Ile Ala Phe Val Ala Val Val Arg Cys Arg Pro Thr Ala
 305 310 315 320
 Phe His Leu Ser Trp Trp Ala Met Val Phe Pro Asn Thr Gly Phe Thr
 325 330 335
 Leu Ala Thr Ile Thr Leu Gly Arg Ala Leu Gly Ser Pro Gly Val Leu
 340 345 350
 Gly Val Gly Ser Ala Met Ser Val Gly Val Val Cys Met Trp Val Phe
 355 360 365
 Val Phe Val Tyr His Ile Arg Ala Val Ile Arg Gln Asp Ile Met Tyr
 370 375 380
 Pro Gly Lys Asp Glu Asp Val Leu Asp
 385 390

<210> SEQ ID NO 44

<211> LENGTH: 1294

<212> TYPE: DNA

<213> ORGANISM: *Aspergillus oryzae*

<400> SEQUENCE: 44

```

atgttcgctg ctcgccagtc tttcaacctc ctccagaagc gcgccttctc cgctctgcc      60
agccagggtg gtgattgaat ggatccattg gacctcggag ctacctctgc aacatcaaca      120
aaactaacat actaacttat cttcttcata ggcttccaag gttgccgttc ttggtgccgc      180
tggtggcatt ggccagcctc tctcccttct cctcaagctc aacccccgtg tttctgagct      240
tgccctctac gatatccgcg gtggcccttg tatgtttttg cacagcttgc aacatctccg      300
acttcggtga ttcaagacag ggctaacata aggatacaat aggtgttgcc gctgacctga      360
gccacatcaa caccaacagc accgtctctg gctacgaggc taccctctct ggctccgtg      420
atgctctcaa gggctccgag atcgctctca tccctgccgg tgttctctgc aagcccgga      480
tgaccgtga cggtatgaac cgtaacttg tcaatggcac tgggaattga atactaatta      540
taatatcgcc agacctgttc aacaccaacg cctccattgt ccgcgacctt gctaaggccg      600
ccgccgaggc ttcccccgag gccaacatcc tcgtcatctc caacctgtga tgacgctttc      660
caccactgc taccagttat ctgcgcgctaa ttgcaatcag gtcaactcca ccgtcccat      720
cgtctctgag gtcttcaagt ccaagggtgt ctacaacccc aagcgtctct tcggtgtcac      780
tacccttgac gttgtccgtg cctctcgtct catctcccag gtccagaaga ccgacctc      840
caacgaggcc gtcactgtcg tcggtggtca ctccggtgtg accattgtcc ctcttctctc      900
ccagtccagc caccacagca ttgagggtaa gacccgcat gagctcgtca accgcatcca      960
gttcggtggt gatgaggttg tcaaggccaa ggatggtgct ggctctgcca cctctccat      1020
ggccatggct ggtgctcgca tgctgagtc cctcctgaag gccgcccagg gtgagaaggg      1080
tgctgttag cccactttcg tcgacagccc tctctacaag gaccagggtg ttgacttctt      1140

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cgccctccaag gtcgagctcg gcccacaacgg tgttgagaag atctctccccg ttggccaggt 1200
caacgcctac gaggagaagc tctctgaggc ctgccttggt gacctcaaga agaacaacca 1260
gaagggtatt gacttcgtca aggccaaccc ttaa 1294

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<210> SEQ ID NO 45
<211> LENGTH: 340
<212> TYPE: PRT
<213> ORGANISM: Aspergillus oryzae

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<400> SEQUENCE: 45

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```

Met Phe Ala Ala Arg Gln Ser Phe Asn Leu Leu Gln Lys Arg Ala Phe
 1             5             10            15

Ser Ala Ser Ala Ser Gln Ala Ser Lys Val Ala Val Leu Gly Ala Ala
 20            25            30

Gly Gly Ile Gly Gln Pro Leu Ser Leu Leu Leu Lys Leu Asn Pro Arg
 35            40            45

Val Ser Glu Leu Ala Leu Tyr Asp Ile Arg Gly Gly Pro Gly Val Ala
 50            55            60

Ala Asp Leu Ser His Ile Asn Thr Asn Ser Thr Val Ser Gly Tyr Glu
 65            70            75            80

Ala Thr Pro Ser Gly Leu Arg Asp Ala Leu Lys Gly Ser Glu Ile Val
 85            90            95

Leu Ile Pro Ala Gly Val Pro Arg Lys Pro Gly Met Thr Arg Asp Asp
100            105            110

Leu Phe Asn Thr Asn Ala Ser Ile Val Arg Asp Leu Ala Lys Ala Ala
115            120            125

Ala Glu Ala Ser Pro Glu Ala Asn Ile Leu Val Ile Ser Asn Pro Val
130            135            140

Asn Ser Thr Val Pro Ile Val Ser Glu Val Phe Lys Ser Lys Gly Val
145            150            155            160

Tyr Asn Pro Lys Arg Leu Phe Gly Val Thr Thr Leu Asp Val Val Arg
165            170            175

Ala Ser Arg Phe Ile Ser Gln Val Gln Lys Thr Asp Pro Ser Asn Glu
180            185            190

Ala Val Thr Val Val Gly Gly His Ser Gly Val Thr Ile Val Pro Leu
195            200            205

Leu Ser Gln Ser Ser His Pro Ser Ile Glu Gly Lys Thr Arg Asp Glu
210            215            220

Leu Val Asn Arg Ile Gln Phe Gly Gly Asp Glu Val Val Lys Ala Lys
225            230            235            240

Asp Gly Ala Gly Ser Ala Thr Leu Ser Met Ala Met Ala Gly Ala Arg
245            250            255

Met Ala Glu Ser Leu Leu Lys Ala Ala Gln Gly Glu Lys Gly Val Val
260            265            270

Glu Pro Thr Phe Val Asp Ser Pro Leu Tyr Lys Asp Gln Gly Val Asp
275            280            285

Phe Phe Ala Ser Lys Val Glu Leu Gly Pro Asn Gly Val Glu Lys Ile
290            295            300

Leu Pro Val Gly Gln Val Asn Ala Tyr Glu Glu Lys Leu Leu Glu Ala
305            310            315            320

Cys Leu Gly Asp Leu Lys Lys Asn Ile Gln Lys Gly Ile Asp Phe Val
325            330            335

Lys Ala Asn Pro

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<400> SEQUENCE: 54

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<210> SEQ ID NO 55
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<400> SEQUENCE: 55

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<210> SEQ ID NO 56
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<400> SEQUENCE: 56

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<210> SEQ ID NO 57
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What is claimed is:

1. A recombinant fungal or prokaryotic host cell comprising a heterologous polynucleotide encoding a bicarbonate transporter, wherein the heterologous polynucleotide:

- (a) encodes a bicarbonate transporter having at least 90% sequence identity to SEQ ID NO: 4; or
- (b) has at least 90% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof;

wherein the host cell is capable of producing a greater amount of a C4-dicarboxylic acid compared to the host cell without the heterologous polynucleotide when cultivated under the same conditions.

2. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a bicarbonate transporter having at least 90% sequence identity to SEQ ID NO: 4.

3. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a bicarbonate transporter having at least 95% sequence identity to SEQ ID NO: 4.

4. The recombinant host cell of claim 1, wherein the heterologous polynucleotide has at least 90% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof.

5. The recombinant host cell of claim 1, wherein the heterologous polynucleotide has at least 95% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof.

6. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a polypeptide that comprises or consists of SEQ ID NO: 4.

7. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encoding the bicarbonate transporter is operably linked to a promoter foreign to the polynucleotide.

8. The recombinant host cell of claim 1, further comprising a heterologous polynucleotide encoding a C4-dicarboxylic acid transporter.

9. The recombinant host cell of claim 8, wherein the heterologous polynucleotide encoding a C4-dicarboxylic acid transporter is operably linked to a promoter foreign to the polynucleotide.

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10. The recombinant host cell of claim 1, further comprising a heterologous polynucleotide encoding a malate dehydrogenase.

11. The recombinant host cell of claim 10, wherein the heterologous polynucleotide encoding a malate dehydrogenase is operably linked to a promoter foreign to the polynucleotide.

12. The recombinant host cell of claim 1, further comprising a heterologous polynucleotide encoding a pyruvate carboxylase.

13. The recombinant host cell of claim 12, wherein the heterologous polynucleotide encoding a pyruvate carboxylase is operably linked to a promoter foreign to the polynucleotide.

14. The recombinant host cell of claim 13, wherein the host cell is a filamentous fungal host cell.

15. The recombinant host cell of claim 14, wherein the host cell is selected from the group consisting of an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phiebia*, *Piromyces*, *Pleurotus*, *Rhizopus*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trametes*, and *Trichoderma*.

16. The recombinant host cell of claim 14, wherein the host cell is an *Aspergillus* host cell.

17. The recombinant host cell of claim 16, wherein the host cell is an *Aspergillus oryzae* host cell.

18. The recombinant host cell of claim 16, wherein the host cell is an *Aspergillus niger* host cell.

19. The recombinant host cell of claim 1, wherein the C4-dicarboxylic acid is malic acid.

20. The recombinant host cell of claim 1, wherein the host cell is capable of producing a greater amount of the C4-dicarboxylic acid by at least 25% compared to the host cell without the heterologous polynucleotide that encodes the bicarbonate transporter, when cultivated under the same conditions.

21. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a bicarbonate transporter having at least 97% sequence identity to SEQ ID NO: 4.

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22. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a bicarbonate transporter having at least 98% sequence identity to SEQ ID NO: 4.

23. The recombinant host cell of claim 1, wherein the heterologous polynucleotide encodes a bicarbonate transporter having at least 99% sequence identity to SEQ ID NO: 4.

24. The recombinant host cell of claim 1, wherein the heterologous polynucleotide has at least 97% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof.

25. The recombinant host cell of claim 1, wherein the heterologous polynucleotide has at least 98% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof.

26. The recombinant host cell of claim 1, wherein the heterologous polynucleotide has at least 99% sequence identity to SEQ ID NO: 3, or the cDNA sequence thereof.

27. A recombinant *Aspergillus oryzae* host cell comprising a heterologous polynucleotide that encodes a bicarbonate transporter, wherein:

the heterologous polynucleotide is operably linked to a promoter foreign to the polynucleotide;

the heterologous polynucleotide encodes a bicarbonate transporter having at least 95% sequence identity to SEQ ID NO: 4; and

the host cell is capable of producing a greater amount of malic acid compared to the host cell without the heterologous polynucleotide when cultivated under the same conditions.

28. The recombinant host cell of claim 27, wherein the heterologous polynucleotide encodes a bicarbonate transporter that comprises or consists of SEQ ID NO: 4.

29. A method of producing a C4-dicarboxylic acid, comprising:

(a) cultivating the recombinant host cell of claim 1 in a medium under suitable conditions to produce the C4-dicarboxylic acid; and

(b) recovering the C4-dicarboxylic acid.

30. The method of claim 29, wherein the C4-dicarboxylic acid is malic acid.

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